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OM nucleic - nucleic search, using sw model

Run on: July 8, 2004, 09:55:09 ; Search time 565.265 Seconds  
(without alignments)  
10351.438 Million cell updates/sec

Title: US-10-025-145A-3\_COPY\_1560\_1694  
Perfect score: 135  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	135	100.0	533	6	AR222113	AR222113 Sequence
2	135	100.0	2018	6	BD2227661	BD2227661 Synthases
3	135	100.0	2018	6	AR222097	AR222097 Sequence
4	135	100.0	2018	6	AR240696	AR240696 Sequence
5	135	100.0	2018	6	AR266971	AR266971 Sequence
6	135	100.0	2018	6	AR316320	AR316320 Sequence
7	135	100.0	2018	6	AR338463	AR338463 Sequence
8	135	100.0	2018	6	AR429869	AR429869 Sequence
9	135	100.0	2018	8	AGU87909	U87909 Abies grand
10	119	88.1	1958	8	AY237645	AY237645 Picea sit
11	115.8	85.8	2082	8	AF543527	AF543527 Pinus tae
12	114.2	84.6	2013	6	AR222136	AR222136 Sequence
13	114.2	84.6	2013	8	AGU87910	U87910 Abies grand
14	112.6	83.4	2089	6	BD227677	BD227677 Synthases
15	112.6	83.4	2089	6	AR222098	AR222098 Sequence
16	112.6	83.4	2089	6	AR240712	AR240712 Sequence
17	112.6	83.4	2089	6	AR266987	AR266987 Sequence
18	112.6	83.4	2089	6	AR316336	AR316336 Sequence
19	112.6	83.4	2089	6	AR338479	AR338479 Sequence
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31	104.6	77.5	2196	6	AR240701	AR240701 Sequence
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33	104.6	77.5	2196	6	AR316325	AR316325 Sequence
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37	104.6	77.5	2205	6	AR222116	AR222116 Sequence
38	104	77.0	3306	8	AF326517	AF326517 Abies gra
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ALIGNMENTS

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DEFINITION Sequence 24 from patent US 6429014.  
ACCESSION AR222113  
VERSION AR222113.1 GI:23329487  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 533)  
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.  
TITLE Monoterpene synthases from grand fir (Abies grandis)  
JOURNAL Patent: US 6429014-A 24 06-AUG-2002;  
FEATURES Location/Qualifiers

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DEFINITION Synthesizes.
ACCESSION  BD227661
VERSION    BD227661.1 GI:33037431
KEYWORDS   JP 2002526066-A/13.
SOURCE     Abies grandis
ORGANISM   Abies grandis
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            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
REFERENCE  1 (bases 1 to 2018)
AUTHORS   Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE     Synthesizes
JOURNAL   Patent: JP 2002526066-A 13 20-AUG-2002;
            UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR
            BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN
            SERVICES
COMMENT    OS Abies grandis (giant fir)
            PN JP 2002526066-A/13
            PD 20-AUG-2002
            PF 17-SEP-1999 JP 2000574228
            PR 18-SEP-1998 US 60/100993,22-APR-1999 US 60/130628 PR
            23-AUG-1999 US 60/150262
            PI JOSEPH CHAPPELL,KATHLEEN R MANNA,JOSEPH P NOEL,COURTNEY M PI
            STARKS
            PC C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/
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            PC C12Q1/25,G01N33/68// (C12N9/12,C12R1:91), (C12N9/12,C12R1:19),
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            PC C12N5/00,C12N5/00
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            FT CDS
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Db      1680 CATATCAACGCCCATG 1694

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LOCUS      AR222097
DEFINITION Sequence 3 from patent US 6429014.
ACCESSION  AR222097
VERSION    AR222097.1 GI:23329471
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
            1 (bases 1 to 2018)
REFERENCE  Steele,C.L., Bohlmann,J. and Croteau,R.B.
AUTHORS   Monoterpene synthases from grand fir (Abies grandis)
TITLE     Patent: US 6429014-A 3 06-AUG-2002;
JOURNAL   Location/Qualifiers
FEATURES   source
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Qy      121 CATATCAACGCCCATG 135
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Db      1680 CATATCAACGCCCATG 1694

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LOCUS      AR240696
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ACCESSION  AR240696
VERSION    AR240696.1 GI:27285845
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
            1 (bases 1 to 2018)
REFERENCE  Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
AUTHORS   Methods of making modified polypeptides
TITLE     Patent: US 6468772-A 19 22-OCT-2002;
JOURNAL   Location/Qualifiers
FEATURES   source
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RESULT 5  
AR266971  
LOCUS AR266971 2018 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 19 from patent US 6495354.  
ACCESSION AR266971  
VERSION AR266971.1 GI:29696426  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Syntheses  
JOURNAL Patent: US 6495354-A 19 17-DEC-2002;  
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LOCUS AR316320 2018 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 19 from patent US 6559297.  
ACCESSION AR316320  
VERSION AR316320.1 GI:31711055  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Syntheses  
JOURNAL Patent: US 6559297-A 19 06-MAY-2003;  
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Db 1680 CATATCAACGCCATG 1694  
  
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LOCUS AR338463 2018 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 19 from patent US 6569656.  
ACCESSION AR338463  
VERSION AR338463.1 GI:33725240  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Syntheses  
JOURNAL Patent: US 6569656-A 19 27-MAY-2003;  
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QY 121 CATATCAACGCCATG 135  
Db 1680 CATATCAACGCCATG 1694  
  
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LOCUS AR429869 2018 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 19 from patent US 6645762.  
ACCESSION AR429869  
VERSION AR429869.1 GI:40190267  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Syntheses  
JOURNAL Patent: US 6645762-A 19 11-NOV-2003;  
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RESULT 9  
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LOCUS AGU87909 2018 bp mRNA linear PLN 24-SEP-1997  
DEFINITION Abies grandis pinene synthase (AG3.18) mRNA, complete cds.  
ACCESSION U87909  
VERSION U87909.1 GI:2411482  
KEYWORDS  
SOURCE  
ORGANISM Abies grandis  
Abies grandis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Bohlmann, J., Steele, C.L. and Croteau, R.  
TITLE Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase  
JOURNAL J. Biol. Chem. 272 (35), 21784-21792 (1997)  
MEDLINE 97413772  
PubMed 9268308  
REFERENCE 2 (bases 1 to 2018)  
AUTHORS Bohlmann, J., Steele, C.L. and Croteau, R.  
TITLE Direct Submission  
JOURNAL Submitted (31-JAN-1997) Institute of Biological Chemistry, Washington State University, Clark Hall, Pullman, WA 99164-6340, USA

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RESULT 10  
AY237645  
LOCUS AY237645 1958 bp mRNA linear PLN 13-SEP-2003  
DEFINITION Picea sitchensis pinene synthase mRNA, complete cds.  
ACCESSION AY237645  
VERSION AY237645.1 GI:34582666  
KEYWORDS  
SOURCE  
ORGANISM Picea sitchensis (Sitka spruce)  
Picea sitchensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
REFERENCE 1 (bases 1 to 1958)  
AUTHORS Byun McKay, S.A., Hunter, W.L., Godard, K.A., Wang, S.X., Martin, D.M., Bohlmann, J. and Plant, A.L.  
TITLE Insect Attack and Wounding Induce Traumatic Resin Duct Development and Gene Expression of (-)-Pinene Synthase in Sitka Spruce  
JOURNAL Plant Physiol. 133 (1), 368-378 (2003)  
PubMed 12970502  
REFERENCE 2 (bases 1 to 1958)  
AUTHORS Byun McKay, A.S., Hunter, W.L., Goddard, K.A., Wang, S.X., Martin, D., Bohlmann, J. and Plant, A.L.  
TITLE Direct Submission  
JOURNAL Submitted (17-FEB-2003) Biology, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada  
FEATURES  
source Location/Qualifiers  
1. .1958  
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75. .1958  
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PQMTFCRHRHVEYYTLASCIAPFQHSGRFRLGFAKACHIIITLDDMYDTFGTVDELEL  
FTAMKRWDPSAADCLPEYMKGVYLLIYDTVNETSREAEKAQGRDILDYARRAWDDYL  
DSYMQEAKWIATGYLPTFAEYYENGKVSSSHRTSALQPILTMDIPPPHILKEVDFFS  
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VTL"

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Best Local Similarity 92.6%; Pred. No. 2.5e-28;  
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Db 1626 CTTCGACTACGAGGTGATACGCGGTGCTACAAGCGGACAGAGCCCGTGGAGAGAAGCT 1685  
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Db 1686 TCTAGTATATCTTGTATTATGAAGACAAATCCTGGAGCAACAGAGGAAGATGCTCTCGAC 1745  
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Db 1746 CATATCAACGCCATG 1760  
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AF543527  
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DEFINITION Pinus taeda (-)-alpha-pinene synthase mRNA, complete cds.  
ACCESSION AF543527  
VERSION AF543527.1 GI:28894481  
KEYWORDS  
SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
REFERENCE 1 (bases 1 to 2082)  
AUTHORS Phillips,M.A., Wildung,M.R., Williams,D.C., Hyatt,D.C. and  
Croteau,R.  
TITLE cDNA isolation, functional expression, and characterization of  
(+)-alpha-pinene synthase and (-)-alpha-pinene synthase from  
loblolly pine (Pinus taeda): Stereocontrol in pinene biosynthesis  
JOURNAL Arch. Biochem. Biophys. 411 (2), 267-276 (2003)  
MEDLINE 22510022  
PUBMED 12623076  
REFERENCE 2 (bases 1 to 2082)  
AUTHORS Phillips,M.A., Wildung,M.R., Williams,D.C. and Croteau,R.B.  
TITLE Direct Submission  
JOURNAL Submitted (09-SEP-2002) Institute of Biological Chemistry,  
Washington State University, PO Box 646340, Pullman, WA 99164-6340,  
USA  
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source Location/Qualifiers  
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32..1921  
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RTVLNLYRASLIAEPGEKVMDEAESFSAKYLKEALQKIPVSSFSREIGDVLEYGHTY  
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GSPQMTFCRRHRHVEYYTLASCIAPFPQHSGRFLGFAKACHIIITVLDDMYDTFGTLDL  
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DVIKGLNWELLKPNSSVPISAKXHAFDISRAFHCGYKYRDGYSVAN IETKSLVKRTVI  
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Best Local Similarity 91.1%; Pred. No. 2.9e-27;  
Matches 123; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 CTTTCGATTACGAGGTGATACGCGGTGCTACAAAGCGGACAGGGCTCGTGGAGAAGCT 60  
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Db 1709 CATCTCAACGCCATG 1723  
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RESULT 12

AR222136  
LOCUS AR222136 2013 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 64 from patent US 6429014.  
ACCESSION AR222136  
VERSION AR222136.1 GI:23329510  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2013)  
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.  
TITLE Monoterpene synthases from grand fir (Abies grandis)  
JOURNAL Patent: US 6429014-A 64 06-AUG-2002;  
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AGU87910  
LOCUS AGU87910 2013 bp mRNA linear PLN 10-AUG-2001  
DEFINITION Abies grandis (-)-camphene synthase (AG6.5) mRNA, complete cds.  
ACCESSION U87910  
VERSION U87910.1 GI:2411484  
KEYWORDS  
SOURCE Abies grandis  
ORGANISM Abies grandis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.  
REFERENCE 1 (bases 1 to 2013)  
AUTHORS Bohlmann,J., Steele,C.L. and Croteau,R.  
TITLE Monoterpene synthases from grand fir (Abies grandis). cDNA  
isolation, characterization, and functional expression of myrcene  
synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene  
synthase  
JOURNAL J. Biol. Chem. 272 (35), 21784-21792 (1997)  
MEDLINE 97413772  
PUBMED 9268308  
REFERENCE 2 (bases 1 to 2013)  
AUTHORS Bohlmann,J., Phillips,M., Ramachandiran,V., Kato,H., S. and Croteau,R.  
TITLE cDNA cloning, characterization, and functional expression of four  
new monoterpene synthase members of the Tpsd gene family from grand  
fir (Abies grandis)  
JOURNAL Arch. Biochem. Biophys. 368 (2), 232-243 (1999)  
MEDLINE 99373092  
PUBMED 10441373  
REFERENCE 3 (bases 1 to 2013)  
AUTHORS Bohlmann,J., Steele,C.L. and Croteau,R.  
TITLE Direct Submission  
JOURNAL Submitted (31-JAN-1997) Institute of Biological Chemistry,  
Washington State University, Clark Hall, Pullman, WA 99164-6340,  
USA  
FEATURES  
source Location/Qualifiers  
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CDS

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Best Local Similarity 90.4%; Pred. No. 9.7e-27;
Matches 122; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 61 TCCTCTATATCATGTTATATGAAAGACAAATCCTCGAGTATCAGAGGAAGATGCTCTCGAT 120
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QY 121 CATATCAACGCCATG 135
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RESULT 14
BD227677
LOCUS BD227677 2089 bp DNA linear PAT 17-JUL-2003
DEFINITION Synthesizes.
ACCESSION BD227677
VERSION BD227677.1 GI:33037447
KEYWORDS JP 2002526066-A/29.
SOURCE Abies grandis
ORGANISM Abies grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
1 (bases 1 to 2089)
Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
Synthases
Patent: JP 2002526066-A 29 20-AUG-2002;
UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR
BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN
SERVICES
OS Abies grandis (giant fir)
PN JP 2002526066-A/29
PD 20-AUG-2002
PF 17-SEP-1999 JP 2000574228
PR 18-SEP-1998 US 60/100993,22-APR-1999 US 60/130628 PR
23-AUG-1999 US 60/150262
PI JOSEPH CHAPPELL,KATHLEEN R MANNA,JOSEPH P NOEL,COURTNEY M PI
STARKS
PC C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/
PC 10,C12N9/12,
PC C12Q1/25,G01N33/68// (C12N9/12,C12R1:91), (C12N9/12,C12R1:19),
PC C12N15/00,
PC C12N5/00,C12N5/00
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CC (-)-4S-limonene synthase
FH Key Location/Qualifiers
FT CDS (73)..(1983).

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QY 121 CATATCAACGCCATG 135
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RESULT 15
AR222098
LOCUS AR222098 2089 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 5 from patent US 6429014.
ACCESSION AR222098
VERSION AR222098.1 GI:23329472
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2089)
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.
TITLE Monoterpene synthases from grand fir (Abies grandis)
JOURNAL Patent: US 6429014-A 5 06-AUG-2002;
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Best Local Similarity 89.6%; Pred. No. 3.3e-26;
Matches 121; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGGCGGACAGGGCTCGTGGAGAAGAGCT 60
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QY 61 TCCTCTATATCATGTTATATGAAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120
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QY 121 CATATCAACGCCATG 135
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Job time : 567.265 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 8, 2004, 09:46:39 ; Search time 61.0265 Seconds  
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Searched: 3373863 seqs, 2124099041 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
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8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	135	100.0	533	2	AAX08660 Probe for
2	135	100.0	533	4	AAF73388 Grand fir
3	135	100.0	2018	2	AAX08644 Pinene sy
4	135	100.0	2018	3	AAA38922 Grand fir
5	135	100.0	2018	4	AAF73372 Grand fir
6	114.2	84.6	2013	4	AAF73411 Grand fir
7	112.6	83.4	2089	2	AAX08645 Limonene
8	112.6	83.4	2089	3	AAA38938 Grand fir
9	112.6	83.4	2089	4	AAF73373 Grand fir
10	111	82.2	2429	4	AAF73413 Grand fir
11	106.2	78.7	1513	3	AAA69551 Pinus rad
12	106.2	77.7	1634	3	AAA69644 Pinus rad
13	104.6	77.5	2196	2	AAX08643 Myrcene s
14	104.6	77.5	2196	3	AAA38927 Grand fir
15	104.6	77.5	2196	4	AAF73371 Grand fir
16	104.6	77.5	2205	2	AAX08663 Grand Fir
17	104.6	77.5	2205	4	AAF73391 Grand fir
18	103	76.3	696	4	AAF73414 Grand fir
19	103	76.3	1890	4	AAF73421 Grand fir
20	99.8	73.9	2186	4	AAF73412 Grand fir
21	96.6	71.6	1173	3	AAA69643 Pinus rad
22	66	48.9	622	2	AAX87526 Grand fir
23	66	48.9	2424	2	AAX08654 Grand Fir

24	66	48.9	2424	3	AAA38932	Aaa38932 Grand fir
25	66	48.9	2424	4	AAF73382	Aaf73382 Grand fir
26	66	48.9	2525	2	AAX87530	Aax87530 E-alpha-b
27	66	48.9	2528	2	AAX87529	Aax87529 Grand fir
28	66	48.9	2528	2	AAX87531	Aax87531 E-alpha-b
29	66	48.9	2571	2	AAX87504	Aax87504 Grand fir
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31	56.4	41.8	2700	3	AAA38931	Aaa38931 Yew taxad
32	52.6	39.0	824	3	AAA69540	Aaa69540 Pinus rad
33	52.6	39.0	1865	3	AAA38933	Aaa38933 Grand fir
34	52.6	39.0	1885	2	AAX87532	Aax87532 Delta-sel
35	52.6	39.0	1885	2	AAX87534	Aax87534 Delta-sel
36	52.6	39.0	1885	2	AAX87533	Aax87533 Delta-sel
37	52.6	39.0	1888	2	AAX87505	Aax87505 Grand fir
38	52.6	39.0	1967	2	AAX87513	Aax87513 Grand fir
39	52.6	39.0	1967	2	AAX08655	Aax08655 Grand Fir
40	52.6	39.0	1967	4	AAF73383	Aaf73383 Grand fir
41	51.6	38.2	2861	3	AAA38937	Aaa38937 Grand fir
42	35.6	26.4	1416	2	AAX08656	Aax08656 Grand Fir
43	35.6	26.4	1416	4	AAF73384	Aaf73384 Grand fir
44	35.6	26.4	1785	2	AAX87536	Aax87536 Gamma-hum
45	35.6	26.4	1785	2	AAX87537	Aax87537 Gamma-hum

ALIGNMENTS

RESULT 1  
AAX08660  
ID AAX08660 standard; DNA; 533 BP.  
XX  
AC AAX08660;  
XX  
DT 27-SEP-1999 (first entry)  
XX  
DE Probe for identifying monoterpene synthase sequences.  
XX  
KW Myrcene synthase; limonene synthase; pinene synthase; flavour;  
KW monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;  
KW ss.  
XX  
OS Abies grandis.  
XX  
PN WO9902030-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014528.  
XX  
PR 11-JUL-1997; 97US-0052249P.  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Bohlmann J, Steele CL, Croteau RB;  
XX  
DR WPI; 1999-120396/10.  
XX  
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. myrcene, limonene or pinene.  
XX  
PS Example 1; Page 10; 121pp; English.  
XX  
CC Nucleotide sequences encoding myrcene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by myrcene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal. cDNAs encoding myrcene



CC synthase, pinene synthase and limonene synthase from Grand Fir were  
CC isolated and sequenced by the following procedure. Based on comparison of  
CC sequences of different plant synthase enzymes, four conserved sequences  
CC were identified for construction of four degenerate primers (AAX08646-  
CC 49). One of these primers (AAX08648) was an antisense primer and used for  
CC PCR with the other three sense primers. Only a combination of primers  
CC AAX08648 and AAX08649 generated a PCR product which was 110 base pairs in  
CC length. The amplified product was used in a plasmid construct to  
CC transform E.coli XL1-Blue cells and the inserts were sequenced. Four  
CC probes (AAX08650-53) were devised from the sequenced insert and were used  
CC to screen a Grand Fir cDNA library. One of these clones is the myrcene  
CC synthase sequence given in AAX08643. The other clones identified are  
CC described in AAX08654-56. Based on comparison of these clones three new  
CC conserved sequences were identified for construction of three degenerate  
CC primers (AAX08657-59). A combination of primers AAX08657 and AAX08659  
CC generated a PCR product which was approximately 1020 base pairs in  
CC length. The amplified product was used in a plasmid construct to  
CC transform E.coli XL1-Blue cells and the inserts were sequenced. The  
CC sequence was identical in all transformants and used as a probe  
CC (AAX08660) to screen a Grand Fir cDNA library. Clones were subcloned  
CC using the primers described in AAX08664-X08669 and then sequenced using  
CC the T3 promoter primer (AAX08661) and T7 promoter primer (AAX08662).  
CC Clones which afforded weak hybridisation to the probe sequence were  
CC identical to the myrcene synthase sequence given in AAX08643. Clones  
CC which gave strong hybridisation signals fell into two distinct groups  
CC represented by the sequences encoding either limonene synthase (AAX08644)  
CC or pinene synthase (AAX08645)

XX  
SQ Sequence 533 BP; 164 A; 116 C; 120 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 135; DB 2; Length 533;  
Best Local Similarity 100.0%; Pred. No. 4.9e-36;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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369 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAGCT 428

QY 61 TCCTCTATATCATGTTATATGAAGACAATCCTCGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
429 TCCTCTATATCATGTTATATGAAGACAATCCTCGAGTATCAGAGGAAGATGCTCTCGAT 488

QY 121 CATATCAACGCCATG 135  
Db ||||||||||||||||  
489 CATATCAACGCCATG 503

RESULT 2  
AAF73388  
ID AAF73388 standard; DNA; 533 BP.  
XX  
AC AAF73388;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir monoterpene synthases probe #3 SEQ ID NO: 24.  
XX

KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; probe;  
KW terpinolene synthase; insect resistance; nutrition; PCR primer; ss.

XX Abies grandis.  
OS  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX

PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;

XX  
DR WPI; 2001-182782/18.

XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.

XX  
PS Example 1; Page 133; 175pp; English.

XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants

XX  
SQ Sequence 533 BP; 164 A; 116 C; 120 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 135; DB 4; Length 533;  
Best Local Similarity 100.0%; Pred. No. 4.9e-36;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAGCT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
369 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAGCT 428

QY 61 TCCTCTATATCATGTTATATGAAGACAATCCTCGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
429 TCCTCTATATCATGTTATATGAAGACAATCCTCGAGTATCAGAGGAAGATGCTCTCGAT 488

QY 121 CATATCAACGCCATG 135  
Db ||||||||||||||||  
489 CATATCAACGCCATG 503

RESULT 3  
AAX08644  
ID AAX08644 standard; cDNA; 2018 BP.

XX  
AC AAX08644;  
XX  
DT 27-SEP-1999 (first entry)  
XX

DE Pinene synthase gene.

XX Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.

OS Abies grandis.

XX  
FH Key Location/Qualifiers  
FT CDS 6.1892  
FT /\*tag= a  
FT /product= "pinene synthase"

XX WO9902030-A1.

PN 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014528.

XX 11-JUL-1997; 97US-0052249P.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Bohlmann J, Steele CL, Croteau RB;

XX WPI; 1999-120396/10.

DR P-PSDB; AAW85701.

XX

PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. mycrene, limonene or pinene.  
XX  
PS Claim 10; Page 74-77; 121pp; English.  
XX  
CC Nucleotide sequences encoding mycrene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by mycrene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal  
XX  
SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;  
Query Match 100.0%; Score 135; DB 2; Length 2018;  
Best Local Similarity 100.0%; Pred. No. 7.9e-36;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGAGAAGCT 60  
Db 1560 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGAGAAGCT 1619  
QY 61 TCCTCTATATCATGTTATATGAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db 1620 TCCTCTATATCATGTTATATGAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 1679  
QY 121 CATATCAACGCCATG 135  
Db 1680 CATATCAACGCCATG 1694  
RESULT 4  
AAA38922  
ID AAA38922 standard; DNA; 2018 BP.  
XX  
AC AAA38922;  
XX  
DT 25-AUG-2000 (first entry)  
XX  
DE Grand fir pinene synthase DNA sequence SEQ ID NO:19.  
XX  
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;  
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;  
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;  
KW defensive agent; pigment; antitumour; steroid hormone;  
KW signal transduction pathway; bile acid; affinity purification;  
KW photoreceptor; enzymatic synthesis; nutrient supplement;  
KW immunological reagent; ds.  
XX  
OS Abies grandis.  
XX  
PN WO200017327-A2.  
XX  
PD 30-MAR-2000.  
XX  
XX 17-SEP-1999; 99WO-US021419.  
XX  
PR 18-SEP-1998; 98US-0100993P.  
PR 22-APR-1999; 99US-0130628P.  
PR 23-AUG-1999; 99US-0150262P.  
XX  
PA (KENT ) UNIV KENTUCKY RES DEPT.  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Chappell J, Manna KR, Noel JP, Starks CM;  
XX  
DR WPI; 2000-292839/25.  
DR P-PSDB; AAY90837.

XX Novel terpene synthase enzymes, useful for producing terpene  
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known  
PT enzymes by specific amino acid alterations.  
XX  
PS Disclosure; Page 363-366; 450pp; English.  
XX  
CC The present invention describes an isolated terpene synthase (I)  
CC comprising a region with at least 20% identity to region 265-535 of a 548  
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha  
CC -carbon atoms (alphaC) that have interatomic distances, between each  
CC other, within tabulated ranges, have a centre point (within a sphere of  
CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered  
CC arrangement of R groups (defining aa side chains), excluding specific  
CC tabulated arrangements (tables given in the specification). (I), and  
CC related enzymes, are used to produce a wide range of terpenoids (e.g.  
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,  
CC flavours, pheromones, defensive agents, pigments, antitumour agents,  
CC components of signal transduction pathways, precursors of steroid  
CC hormones and bile acids, as photoreceptors and as co-factor side chains.  
CC Some synthases with little or no catalytic activity (and nucleic acids  
CC encoding them) are used as controls in the analysis of products formed by  
CC enzymatic synthesis; as nutrient supplements; for affinity purification  
CC of isoprenoids; or to develop immunological reagents or nucleic acids for  
CC monitoring expression of terpene synthase or inheritance of the gene in  
CC plant breeding programs. The new synthases may produce novel terpene  
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;  
Query Match 100.0%; Score 135; DB 3; Length 2018;  
Best Local Similarity 100.0%; Pred. No. 7.9e-36;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGAGAAGCT 60  
Db 1560 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGAGAAGCT 1619  
QY 61 TCCTCTATATCATGTTATATGAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db 1620 TCCTCTATATCATGTTATATGAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 1679  
QY 121 CATATCAACGCCATG 135  
Db 1680 CATATCAACGCCATG 1694  
RESULT 5  
AAF73372  
ID AAF73372 standard; cDNA; 2018 BP.  
XX  
AC AAF73372;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir (-)-pinene synthase coding sequence SEQ ID NO: 3.  
XX  
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
PI WPI; 2001-182782/18.  
XX P-PSDB; AAB69371.  
DR  
XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
PS Claim 38; Page 108-110; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 135; DB 4; Length 2018;  
Best Local Similarity 100.0%; Pred. No. 7.9e-36;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTTACAAAGCGGACAGGGCTCGTGAGAGAAAGCT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1560 CTTTCGATTACGAGGTGATACGCGGTGCTTACAAAGCGGACAGGGCTCGTGAGAGAAAGCT 1619  
  
QY 61 TCCTCTATATCATGTATATGAAAGACAAATCCTGGAGTATCAGAGGAGATGCTCTCGAT 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1620 TCCTCTATATCATGTATATGAAAGACAAATCCTGGAGTATCAGAGGAGATGCTCTCGAT 1679  
  
QY 121 CATATCAACGCCATG 135  
Db ||||||||||||||||  
1680 CATATCAACGCCATG 1694  
  
RESULT 6  
AAF73411  
ID AAF73411 standard; cDNA; 2013 BP.  
XX  
AC AAF73411;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 64.  
XX  
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
XX  
XX WPI; 2001-182782/18.  
DR P-PSDB; AAB69390.  
XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for

PT treatment of cancer.  
XX  
PS Claim 8; Page 147-149; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 2013 BP; 591 A; 432 C; 464 G; 526 T; 0 U; 0 Other;  
  
Query Match 84.6%; Score 114.2; DB 4; Length 2013;  
Best Local Similarity 90.4%; Pred. No. 1.1e-28;  
Matches 122; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
  
QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTTACAAAGCGGACAGGGCTCGTGAGAGAAAGCT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1560 CTTTCGATTACGAGGTGATACACCGGTGCTTACAAAGGCAGACAGGGCCCGTGAGAGAAAGCT 1619  
  
QY 61 TCCTCTATATCATGTATATGAAAGACAAATCCTGGAGTATCAGAGGAGATGCTCTCGAT 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1620 TCGTCTATATCATGTATATGAAAGACAAATCCTGGATTAACGGAGAGATGCTCTGAAT 1679  
  
QY 121 CATATCAACGCCATG 135  
Db ||||||||||||||||  
1680 CATATCAACTTCATG 1694  
  
RESULT 7  
AAX08645  
ID AAX08645 standard; cDNA; 2089 BP.  
XX  
AC AAX08645;  
XX  
DT 27-SEP-1999 (first entry)  
XX  
DE Limonene synthase gene.  
XX  
KW Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.  
XX  
OS Abies grandis.  
XX  
FH Key Location/Qualifiers  
CDS 73..1986  
FT /\*tag= a  
FT /product= "Limonene synthase"  
FT  
PN WO9902030-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014528.  
XX  
PR 11-JUL-1997; 97US-0052249P.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Bohlmann J, Steele CL, Croteau RB;  
XX  
XX WPI; 1999-120396/10.  
DR P-PSDB; AAW85702.  
XX  
XX New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. myrcene, limonene or pinene.  
XX  
PS Claim 11; Page 79-82; 121pp; English.  
XX

CC Nucleotide sequences encoding mycrene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by mycrene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal  
XX  
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;  
  
Query Match 83.4%; Score 112.6; DB 2; Length 2089;  
Best Local Similarity 89.6%; Pred. No. 3.8e-28;  
Matches 121; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 CTTGATTACGAGGTGATACGGGTGCTACAAAGCGGACAGGGTCTCGTGAGAAGAGCT 60  
||||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 1654 CTTGACTACGAGGTGACACGGCTGCTACAAAGCGGATAGGCCCGTGGAAGAAGCT 1713  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 1714 TCAGCTATATCGTGTATATGAAAGACCACTCCTGGATCAATAGAGGAGATGCTCTCAAT 1773  
  
QY 121 CATATCAACGCCATG 135  
||||| ||||||| |||||||  
Db 1774 CATATCAACGCCATG 1788  
  
RESULT 8  
AA38938  
ID AA38938 standard; DNA; 2089 BP.  
XX  
AC AA38938;  
XX  
DT 25-AUG-2000 (first entry)  
XX  
DE Grand fir limonene synthase DNA sequence SEQ ID NO:57.  
XX  
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;  
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;  
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;  
KW defensive agent; pigment; antitumour; steroid hormone;  
KW signal transduction pathway; bile acid; affinity purification;  
KW photoreceptor; enzymatic synthesis; nutrient supplement;  
KW immunological reagent; ds.  
XX  
OS Abies grandis.  
XX  
PN WO200017327-A2.  
XX  
PD 30-MAR-2000.  
XX  
PF 17-SEP-1999; 99WO-US021419.  
XX  
PR 18-SEP-1998; 98US-0100993P.  
PR 22-APR-1999; 99US-0130628P.  
PR 23-AUG-1999; 99US-0150262P.  
XX  
PA (KENT ) UNIV KENTUCKY RES DEPT.  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Chappell J, Manna KR, Noel JP, Starks CM;  
XX  
DR WPI; 2000-292839/25.  
DR P-PSDB; AAY90859.  
XX  
PT Novel terpene synthase enzymes, useful for producing terpene  
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known  
PT enzymes by specific amino acid alterations.  
XX  
PS Disclosure; Page 445-448; 450pp; English.

XX The present invention describes an isolated terpene synthase (I)  
CC comprising a region with at least 20% identity to region 265-535 of a 548  
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha  
CC -carbon atoms (alphaC) that have interatomic distances, between each  
CC other, within tabulated ranges, have a centre point (within a sphere of  
CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered  
CC arrangement of R groups (defining aa side chains), excluding specific  
CC tabulated arrangements (tables given in the specification). (I), and  
CC related enzymes, are used to produce a wide range of terpenoids (e.g.  
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,  
CC flavours, pheromones, defensive agents, pigments, antitumour agents,  
CC components of signal transduction pathways, precursors of steroid  
CC hormones and bile acids, as photoreceptors and as co-factor side chains.  
CC Some synthases with little or no catalytic activity (and nucleic acids  
CC encoding them) are used as controls in the analysis of products formed by  
CC enzymatic synthesis; as nutrient supplements; for affinity purification  
CC of isoprenoids; or to develop immunological reagents or nucleic acids for  
CC monitoring expression of terpene synthase or inheritance of the gene in  
CC plant breeding programs. The new synthases may produce novel terpene  
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;  
  
Query Match 83.4%; Score 112.6; DB 3; Length 2089;  
Best Local Similarity 89.6%; Pred. No. 3.8e-28;  
Matches 121; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 CTTGATTACGAGGTGATACGGGTGCTACAAAGCGGACAGGGTCTCGTGAGAAGAAGCT 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 1654 CTTGACTACGAGGTGACACGGCTGCTACAAAGCGGATAGGCCCGTGGAAGAAGCT 1713  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||  
Db 1714 TCAGCTATATCGTGTATATGAAAGACCACTCCTGGATCAATAGAGGAAGATGCTCTCAAT 1773  
  
QY 121 CATATCAACGCCATG 135  
||||| ||||||| |||||||  
Db 1774 CATATCAACGCCATG 1788  
  
RESULT 9  
AAF73373  
ID AAF73373 standard; cDNA; 2089 BP.  
XX  
AC AAF73373;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir (-)-limonene synthase coding sequence SEQ ID NO: 5.  
XX  
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
XX  
DR WPI; 2001-182782/18.  
DR P-PSDB; AAB69372.  
XX



PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
PS Claim 33; Page 112-115; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;  
  
Query Match 83.4%; Score 112.6; DB 4; Length 2089;  
Best Local Similarity 89.6%; Pred. No. 3.8e-28;  
Matches 121; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 CTTGATTACGAGGTGATACGCGGTGCTACAGCGGACAGGGCTCGTGAGAGAAGCT 60  
Db 1654 CTTGACTACGAGGTGACACGCGCTGCTACAGCGGATAGGGCCCGTGAGAGAAGCT 1713  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db 1714 TCAGCTATATCGTGTATATGAAAGACCATCCTGGATCAATAGAGGAAGATGCTCTCAAT 1773  
  
QY 121 CATATCAACGCCATG 135  
Db 1774 CATATCAACGCCATG 1788  
  
RESULT 10  
AAF73413  
ID AAF73413 standard; cDNA; 2429 BP.  
XX  
AC AAF73413;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 68.  
XX  
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;  
XX  
DR WPI; 2001-182782/18.  
DR P-PSDB; AAB69392.  
XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
PS Claim 23; Page 156-159; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene

CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 2429 BP; 726 A; 484 C; 512 G; 707 T; 0 U; 0 Other;  
  
Query Match 82.2%; Score 111; DB 4; Length 2429;  
Best Local Similarity 88.9%; Pred. No. 1.4e-27;  
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Db 1616 CTTGCGCTACGTGGTGACACGCGCTGCTACAAGCGGATAGGGCTCGTGAGAGAAGCT 1675  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db 1676 TCAGCTATATCGTGTATATGAAAGACCATCCTGGATCAACAGAGGAAGATGCTCTCAAT 1735  
  
QY 121 CATATCAACGCCATG 135  
Db 1736 CATATCAACGCCATG 1750  
  
RESULT 11  
AAA69551  
ID AAA69551 standard; cDNA; 1513 BP.  
XX  
AC AAA69551;  
XX  
DT 08-NOV-2000 (first entry)  
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DE Pinus radiata pinene synthase cDNA SEQ ID NO:25.  
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KW Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;  
KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;  
KW genome mapping; physical mapping; positional cloning; forestry;  
KW agriculture; medicine; fermentation; plant development; pest resistance;  
KW pinene; myrcene; Monterey pine; ss.  
XX  
OS Pinus radiata.  
XX  
PN WO2000036081-A2.  
XX  
PD 22-JUN-2000.  
XX  
PF 16-DEC-1999; 99WO-NZ000219.  
XX  
PR 17-DEC-1998; 98US-00215504.  
PR 29-JUL-1999; 99US-0146441P.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
PI Havukkala IJ;  
XX  
DR WPI; 2000-431575/37.  
DR P-PSDB; AAB18115.  
XX  
PT New plant polynucleotides encoding polypeptides involved in the  
PT production and modification of isoprenoids, useful in forestry and  
PT agriculture for manipulation of isoprenoid metabolism.  
XX  
PS Claim 1; Page 64; 164pp; English.  
XX  
CC The present invention describes plant polynucleotides encoding  
CC polypeptides involved in the production and modification of isoprenoids,  
CC such as terpenoid and steroid compounds. The polynucleotides are used in  
CC genome mapping, in physical mapping and in positional cloning of genes.  
CC The polynucleotides and polypeptides are useful in forestry and  
CC agriculture for manipulation of isoprenoid metabolism, in medicine for



CC therapeutic effects, including direct application in diseased organisms  
CC or indirect application by transgenic organisms and in fermentation and  
CC chemical processing industries involving isoprenoids. In plant  
CC applications, manipulating isoprenoid pathways or isoprenoid composition  
CC may, for example, affect plant development, pest resistance, and the  
CC value of extractives (e.g. pinene and myrcene). The ubiquitous and varied  
CC roles of isoprenoids make the polynucleotides attractive targets for  
CC biotechnical applications in a variety of fields. AAA69527 to AAA69690  
CC and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus radiata  
CC polynucleotides and proteins used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 1513 BP; 437 A; 316 C; 334 G; 426 T; 0 U; 0 Other;  
  
Query Match 78.7%; Score 106.2; DB 3; Length 1513;  
Best Local Similarity 86.7%; Pred. No. 5.3e-26;  
Matches 117; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
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Db 1057 CTTGATTACGAGGTGACACGGGTGTTACAAGCGGACAGTGTCTGTGAGAGAAGCT 1116  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAAATCCTGGAGTATCAGAGGAGATGCTCTCGAT 120  
Db 1117 TCGTGTATATCGTGTCTATATGAAAGAAATCCCGGTCAACACAGGAAGATGCTCTCCAT 1176  
  
QY 121 CATATCAACGCCATG 135  
Db 1177 CATATCAACGGTATG 1191  
  
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AC AAA69644;  
XX  
DT 08-NOV-2000 (first entry)  
XX  
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KW Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;  
KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;  
KW genome mapping; physical mapping; positional cloning; forestry;  
KW agriculture; medicine; fermentation; plant development; pest resistance;  
KW pinene; myrcene; Monterey pine; ss.  
XX  
OS Pinus radiata.  
XX  
PN WO200036081-A2.  
XX  
PD 22-JUN-2000.  
XX  
PF 16-DEC-1999; 99WO-NZ000219.  
XX  
PR 17-DEC-1998; 98US-00215504.  
PR 29-JUL-1999; 99US-0146441P.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
PI Havukkala IJ;  
XX  
DR WPI; 2000-431575/37.  
DR P-PSDB; AAB18044.  
XX  
PT New plant polynucleotides encoding polypeptides involved in the  
PT production and modification of isoprenoids, useful in forestry and  
PT agriculture for manipulation of isoprenoid metabolism.  
XX  
PS Claim 1; Page 89; 164pp; English.  
XX  
CC The present invention describes plant polynucleotides encoding

CC polypeptides involved in the production and modification of isoprenoids,  
CC such as terpenoid and steroid compounds. The polynucleotides are used in  
CC genome mapping, in physical mapping and in positional cloning of genes.  
CC The polynucleotides and polypeptides are useful in forestry and  
CC agriculture for manipulation of isoprenoid metabolism, in medicine for  
CC therapeutic effects, including direct application in diseased organisms  
CC or indirect application by transgenic organisms and in fermentation and  
CC chemical processing industries involving isoprenoids. In plant  
CC applications, manipulating isoprenoid pathways or isoprenoid composition  
CC may, for example, affect plant development, pest resistance, and the  
CC value of extractives (e.g. pinene and myrcene). The ubiquitous and varied  
CC roles of isoprenoids make the polynucleotides attractive targets for  
CC biotechnical applications in a variety of fields. AAA69527 to AAA69690  
CC and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus radiata  
CC polynucleotides and proteins used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 1634 BP; 485 A; 328 C; 355 G; 466 T; 0 U; 0 Other;  
  
Query Match 78.7%; Score 106.2; DB 3; Length 1634;  
Best Local Similarity 86.7%; Pred. No. 5.4e-26;  
Matches 117; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
QY 1 CTTGATTACGAGGTGATACGGGTGCTTACAAGCGGACAGGGCTCGTGAGAGAAGCT 60  
Db 1057 CTTGATTACGAGGTGACACGGGTGTTACAAGCGGACAGTGTCTGTGAGAGAAGCT 1116  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAAATCCTGGAGTATCAGAGGAGATGCTCTCGAT 120  
Db 1117 TCGTGTATATCGTGTCTATATGAAAGAAATCCCGGTCAACACAGGAAGATGCTCTCCAT 1176  
  
QY 121 CATATCAACGCCATG 135  
Db 1177 CATATCAACGGTATG 1191  
  
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AC AAX08643;  
XX  
DT 27-SEP-1999 (first entry)  
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DE Myrcene synthase gene.  
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KW Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.  
XX  
OS Abies grandis.  
XX  
FH Key Location/Qualifiers  
FT CDS 69..1952  
FT /\*tag= a  
FT /product= "Myrcene synthase"  
XX  
PN WO9902030-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014528.  
XX  
PR 11-JUL-1997; 97US-0052249P.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Bohlmann J, Steele CL, Croteau RB;  
XX WPI; 1999-120396/10.  
DR P-PSDB; AAW85700.  
XX  
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
fir (Abies grandis), used to provide plants with modified production of





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OM nucleic - nucleic search, using sw model

Run on: July 8, 2004, 12:09:59 ; Search time 70.7053 Seconds  
(without alignments)  
9305.868 Million cell updates/sec

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Perfect score: 135  
Sequence: 1 ctctgattacgaggtgatac.....tcgatcatatcaacgccatg 135

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Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	135	100.0	2018	9	US-09-887-586A-19
3	135	100.0	2018	9	US-09-903-012-19
4	135	100.0	2018	10	US-09-900-797-19
5	135	100.0	2018	13	US-09-893-820-19
6	135	100.0	2018	14	US-10-041-007-21
7	135	100.0	2018	15	US-10-025-145A-3
8	114.2	84.6	2013	15	US-10-025-145A-64
9	112.6	83.4	2089	9	US-09-887-586A-57
10	112.6	83.4	2089	9	US-09-903-012-57
11	112.6	83.4	2089	10	US-09-900-797-57
12	112.6	83.4	2089	13	US-09-893-820-57
13	112.6	83.4	2089	14	US-10-041-007-23
14	112.6	83.4	2089	15	US-10-025-145A-5

15	111	82.2	2429	14	US-10-041-007-27	Sequence 27, Appl
16	111	82.2	2429	15	US-10-025-145A-68	Sequence 68, Appl
17	104.6	77.5	2196	9	US-09-887-586A-29	Sequence 29, Appl
18	104.6	77.5	2196	9	US-09-903-012-29	Sequence 29, Appl
19	104.6	77.5	2196	10	US-09-900-797-29	Sequence 29, Appl
20	104.6	77.5	2196	13	US-09-893-820-29	Sequence 29, Appl
21	104.6	77.5	2196	14	US-10-041-007-25	Sequence 25, Appl
22	104.6	77.5	2196	15	US-10-025-145A-1	Sequence 1, Appl
23	104.6	77.5	2205	15	US-10-025-145A-31	Sequence 31, Appl
24	103	76.3	696	15	US-10-025-145A-70	Sequence 70, Appl
25	103	76.3	1890	15	US-10-025-145A-77	Sequence 77, Appl
26	99.8	73.9	2186	15	US-10-025-145A-66	Sequence 66, Appl
27	66	48.9	2424	9	US-09-887-586A-45	Sequence 45, Appl
28	66	48.9	2424	9	US-09-903-012-45	Sequence 45, Appl
29	66	48.9	2424	10	US-09-900-797-45	Sequence 45, Appl
30	66	48.9	2424	13	US-09-893-820-45	Sequence 45, Appl
31	66	48.9	2424	14	US-10-041-007-14	Sequence 14, Appl
32	66	48.9	2424	15	US-10-025-145A-15	Sequence 15, Appl
33	66	48.9	2528	14	US-10-041-007-13	Sequence 13, Appl
34	56.4	41.8	2700	9	US-09-887-586A-43	Sequence 43, Appl
35	56.4	41.8	2700	9	US-09-903-012-43	Sequence 43, Appl
36	56.4	41.8	2700	10	US-09-900-797-43	Sequence 43, Appl
37	56.4	41.8	2700	12	US-10-041-018-363	Sequence 363, App
38	56.4	41.8	2700	13	US-09-893-820-43	Sequence 43, Appl
39	52.6	39.0	1865	9	US-09-887-586A-47	Sequence 47, Appl
40	52.6	39.0	1865	9	US-09-903-012-47	Sequence 47, Appl
41	52.6	39.0	1865	10	US-09-900-797-47	Sequence 47, Appl
42	52.6	39.0	1865	13	US-09-893-820-47	Sequence 47, Appl
43	52.6	39.0	1865	14	US-10-041-007-17	Sequence 17, Appl
44	52.6	39.0	1967	15	US-10-025-145A-17	Sequence 17, Appl
45	51.6	38.2	2861	9	US-09-887-586A-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1  
US-10-025-145A-24  
; Sequence 24, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 533  
; TYPE: DNA  
; ORGANISM: Abies Grandis  
US-10-025-145A-24

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Best Local Similarity 100.0%; Pred. No. 4.7e-37;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TCCTCTATATCATGTTATATGAAGACAAATCCTGGAGTATCAGAGGAGATGCTCTCGAT	120



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Db 489 CATATCAACGCCATG 503

RESULT 2

US-09-887-586A-19  
; Sequence 19, Application US/09887586A  
; Patent No. US20020094556A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094556A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/887,586A  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 2018  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)...(1889)  
; OTHER INFORMATION: pinene synthase  
US-09-887-586A-19

Query Match 100.0%; Score 135; DB 9; Length 2018;  
Best Local Similarity 100.0%; Pred. No. 8.4e-37;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAAGCT 60  
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Db 1680 CATATCAACGCCATG 1694

RESULT 3

US-09-903-012-19  
; Sequence 19, Application US/09903012  
; Patent No. US20020094557A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094557A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/903,012  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,993  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
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; FEATURE:  
; NAME/KEY: CDS  
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; OTHER INFORMATION: pinene synthase  
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QY 61 TCCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
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QY 121 CATATCAACGCCATG 135  
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RESULT 4

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; Sequence 19, Application US/09900797  
; Publication No. US20030087406A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20030087406A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/900,797  
; CURRENT FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: US/09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
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; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)...(1889)  
; OTHER INFORMATION: pinene synthase  
US-09-900-797-19

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Db 1620 TCCTCTATATCATGTTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 1679
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RESULT 5
US-09-893-820-19
; Sequence 19, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
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; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-893-820-19

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Db 1620 TCCTCTATATCATGTTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 1679

QY 121 CATATCAACGCCATG 135
Db 1680 CATATCAACGCCATG 1694

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US-10-041-007-21
; Sequence 21, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
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; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
US-10-041-007-21

Query Match 100.0%; Score 135; DB 14; Length 2018;
Best Local Similarity 100.0%; Pred. No. 8.4e-37;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGGACAGGGCTCGTGGAGAAGAAGCT 60
Db 1560 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGGACAGGGCTCGTGGAGAAGAAGCT 1619

QY 61 TCCTCTATATCATGTTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120
Db 1620 TCCTCTATATCATGTTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 1679

QY 121 CATATCAACGCCATG 135
Db 1680 CATATCAACGCCATG 1694

RESULT 7
US-10-025-145A-3
; Sequence 3, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1892)
; OTHER INFORMATION:
US-10-025-145A-3

Query Match 100.0%; Score 135; DB 15; Length 2018;
Best Local Similarity 100.0%; Pred. No. 8.4e-37;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGGACAGGGCTCGTGGAGAAGAAGCT 60
Db 1560 CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGGACAGGGCTCGTGGAGAAGAAGCT 1619

QY 61 TCCTCTATATCATGTTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120
Db 1620 TCCTCTATATCATGTTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 1679

QY 121 CATATCAACGCCATG 135
Db 1680 CATATCAACGCCATG 1694

RESULT 8
US-10-025-145A-64
; Sequence 64, Application US/10025145A
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Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 64  
; LENGTH: 2013  
; TYPE: DNA  
; ORGANISM: Abies Grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)..(1889)  
; OTHER INFORMATION:  
US-10-025-145A-64

Query Match 84.6%; Score 114.2; DB 15; Length 2013;  
Best Local Similarity 90.4%; Pred. No. 1.7e-29;  
Matches 122; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGCT 60  
Db 1560 CTTTCGATTAAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGGCCCGTGGAGAAGCT 1619  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db 1620 TCGTCTATATCATGTTATATGAAAGACAATCCTGGATTAAACGGAAGAGATGCTCTGAAT 1679  
QY 121 CATATCAACGCCATG 135  
Db 1680 CATATCAACTTCATG 1694

RESULT 9  
US-09-887-586A-57  
; Sequence 57, Application US/09887586A  
; Patent No. US20020094556A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094556A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/887,586A  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 57  
; LENGTH: 2089  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (73)...(1983)

; OTHER INFORMATION: (-)-4S-limonene synthase  
US-09-887-586A-57

Query Match 83.4%; Score 112.6; DB 9; Length 2089;  
Best Local Similarity 89.6%; Pred. No. 6.5e-29;  
Matches 121; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGCT 60  
Db 1654 CTTTCGACTACGAGGTGACACGCGGTGCTACAAGCGGATAGGGCCCGTGGAGAAGCT 1713  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db 1714 TCAGCTATATCGTGTATATGAAAGACCATCCTGGATCAATAGAGGAAGATGCTCTCAAT 1773  
QY 121 CATATCAACGCCATG 135  
Db 1774 CATATCAACGCCATG 1788

RESULT 10  
US-09-903-012-57  
; Sequence 57, Application US/09903012  
; Patent No. US20020094557A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094557A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/903,012  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,993  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 57  
; LENGTH: 2089  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (73)...(1983)  
; OTHER INFORMATION: (-)-4S-limonene synthase  
US-09-903-012-57

Query Match 83.4%; Score 112.6; DB 9; Length 2089;  
Best Local Similarity 89.6%; Pred. No. 6.5e-29;  
Matches 121; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGCT 60  
Db 1654 CTTTCGACTACGAGGTGACACGCGGTGCTACAAGCGGATAGGGCCCGTGGAGAAGCT 1713  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
Db 1714 TCAGCTATATCGTGTATATGAAAGACCATCCTGGATCAATAGAGGAAGATGCTCTCAAT 1773  
QY 121 CATATCAACGCCATG 135  
Db 1774 CATATCAACGCCATG 1788

RESULT 11  
US-09-900-797-57  
; Sequence 57, Application US/09900797



Search completed: July 8, 2004, 17:14:28  
Job time : 71.7053 secs

; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 2089  
; TYPE: DNA  
; ORGANISM: Abies Grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (73)..(1986)  
; OTHER INFORMATION:  
US-10-025-145A-5

Query Match	83.4%;	Score 112.6;	DB 15;	Length 2089;
Best Local Similarity	89.6%;	Pred. No. 6.5e-29;		
Matches 121;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;

  

QY	1	CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAAGCT	60
Db	1654	CTTCGACTACGAGGTGACACGCGCTGCTACAAGCGGATAGGGCCCGTGGAGAAGAAGCT	1713

  

QY	61	TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT	120
Db	1714	TCAGCTATATCGTGTATATGAAAGACCATCCTGGATCAATAGAGGAAGATGCTCTCAAT	1773

  

QY	121	CATATCAACGCCATG	135
Db	1774	CATATCAACGCCATG	1788

RESULT 15  
US-10-041-007-27  
; Sequence 27, Application US/10041007  
; Publication No. US20020164736A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsuda, Seiichi P.T.  
; APPLICANT: Schepmann, Hala G  
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase  
; FILE REFERENCE: P02081US1  
; CURRENT APPLICATION NUMBER: US/10/041,007  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: US 60/259,881  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 2429  
; TYPE: DNA  
; ORGANISM: Abies grandis  
US-10-041-007-27

Query Match	82.2%;	Score 111;	DB 14;	Length 2429;
Best Local Similarity	88.9%;	Pred. No. 2.5e-28;		
Matches 120;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;

  

QY	1	CTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAAGCT	60
Db	1616	CTTCGGCTACGTGGTGACACGCGCTGCTACAAGCGGATAGGGCTCGTGGAGAAGAAGCT	1675

  

QY	61	TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT	120
Db	1676	TCAGCTATATCGTGTATATGAAAGACCATCCTGGATCAACAGAGGAAGATGCTCTCAAT	1735

  

QY	121	CATATCAACGCCATG	135
Db	1736	CATATCAACGTCATG	1750



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 8, 2004, 11:16:49 ; Search time 413.736 Seconds  
(without alignments)  
9743.880 Million cell updates/sec

Title: US-10-025-145A-3\_COPY\_1560\_1694  
Perfect score: 135  
Sequence: 1 cttcgattacgaggtgatac.....tcgatcatatcaacgccatg 135

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_mam: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrl: \*  
28: gb\_gss1: \*  
29: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115.8	85.8	516	13 BQ698077	BQ698077 NXPV 064
2	115.8	85.8	541	14 CF672979	CF672979 RTCNT1_75
3	115.8	85.8	637	14 CF476978	CF476978 RTWW3_5_A
4	115.8	85.8	697	13 BQ196773	BQ196773 NXLV105_B

5	115.8	85.8	745	14	CF477103	CF477103 RTWW3_5_A
6	112.6	83.4	517	13	BX677624	BX677624 BX677624
7	111.8	82.8	599	12	BG526917	BG526917 NXPV 057
8	104.6	77.5	591	14	CA305371	CA305371 hasp004xk
9	104.6	77.5	599	13	BX680641	BX680641 BX680641
10	96.6	71.6	542	10	BG039521	BG039521 NXSI_099
11	96.6	71.6	574	9	AW065088	AW065088 ST39E04_P
12	96.6	71.6	574	14	CF474640	CF474640 RTWW2_7_B
13	96.6	71.6	651	14	CF479884	CF479884 RTWW3_12
14	96.6	71.6	696	14	CF401916	CF401916 RTWW1_15
15	96.6	71.6	700	14	CF474786	CF474786 RTWW2_7_B
16	96.6	71.6	733	14	CF666270	CF666270 RTCNT1_22
17	96.6	71.6	740	14	CF477562	CF477562 RTWW3_8_G
18	88.6	65.6	597	14	CF666416	CF666416 RTCNT1_23
19	88.6	65.6	682	14	CF663768	CF663768 RTCNT1_5
20	74.2	55.0	669	14	CF479802	CF479802 RTWW3_12
21	66.4	49.2	539	10	AW287756	AW287756 EST0004_S
22	61.4	45.5	534	14	CF389058	CF389058 RTDR2_13
23	61.4	45.5	741	14	CF389118	CF389118 RTDR2_13
24	59	43.7	488	14	CF472708	CF472708 RTDS1_11
25	59	43.7	669	14	CF397861	CF397861 RTDS3_23
26	59	43.7	682	14	CF397245	CF397245 RTDS3_2_A
27	55.6	41.2	635	14	CF665839	CF665839 RTCNT1_18
28	51	37.8	400	14	CF672970	CF672970 RTCNT1_75
29	49.8	36.9	730	13	BX682869	BX682869 BX682869
30	49.6	36.7	506	12	BG317597	BG317597 NXPV_003
31	46.2	34.2	567	9	AU299970	AU299970 AU299970
32	40.6	30.1	515	14	CF663952	CF663952 RTCNT1_6
33	36.6	27.1	360	10	AW290355	AW290355 NXNV018D1
34	36.6	27.1	360	14	CD026983	CD026983 NXNV018D1
35	36.2	26.8	485	14	CF470359	CF470359 RTDS1_17
36	35.8	26.5	990	29	CG014635	CG014635 ZUAGK78TV
37	35.6	26.4	380	29	CG999639	CG999639 ZMMBBB053
38	34.8	25.8	414	29	CC757577	CC757577 ZMMBBB014
39	34.8	25.8	619	29	CC826228	CC826228 ZMMBBB017
40	34.8	25.8	633	29	CG848835	CG848835 ZMMBBB033
41	34.8	25.8	688	29	CC875261	CC875261 ZMMBBB018
42	34.8	25.8	745	29	CC740342	CC740342 ZMMBBB010
43	34.8	25.8	799	29	CG884155	CG884155 ZMMBBB049
44	34.6	25.6	690	12	BG591505	BG591505 EST499347
45	34.2	25.3	540	29	CG888779	CG888779 ZMMBBB036

ALIGNMENTS

RESULT 1  
BQ698077  
LOCUS BQ698077 516 bp mRNA linear EST 07-MAY-2003  
DEFINITION NXPV\_064\_C05\_F\_NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda  
CDNA\_clone NXPV\_064\_C05\_5' similar to Arabidopsis thaliana sequence  
Atlg61680 hypothetical protein see  
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.  
ACCESSION BQ698077  
VERSION BQ698077.1 GI:21823393  
KEYWORDS EST.  
SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
1 (bases 1 to 516)  
AUTHORS Sederoff, R.  
TITLE Molecular Basis of Wood Formation in the Pine Megagenome  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron\_sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further

information.  
Seq primer: T3.  
Location/Qualifiers  
1. .516  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXPV\_064 C05"  
/tissue\_type="Xylem"  
/cell\_type="Planings (secondary)"  
/dev\_stage="Transitional"  
/lab\_host="XL1-Blue"  
/clone\_lib="NXPV (Nsf Xylem Planings wood Vertical)"  
/note="Vector: Bluescript SK; Site\_1: Eco RI; Site\_2: XhoI; The library is from early (spring) secondary wood, taken from a ten year old tree in the transitional phase. The tree is a kind gift of the Westvaco Corporation. Secondary xylem was harvested from the tree by peeling back the bark and primary xylem and then removing the underlying tissue with a block plane. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."

ORIGIN

Query Match 85.8%; Score 115.8; DB 13; Length 516;  
Best Local Similarity 91.1%; Pred. No. 4.6e-27;  
Matches 123; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 CTTGATTACGAGGTGATACGGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGACT 60  
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Db 209 CTTGATTACGAGGGGATACGGCTGCTACAGCGGACAGGGCCCCGTGGAGAAGACT 268  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
|||  
Db 269 TCGTGTATATCTTGTATATGAAAGACAATCCTGGAACAACAGAGGAAGATGCTCTCAAT 328  
  
QY 121 CATATCAACGCCATG 135  
|||  
Db 329 CATCTCAACGCCATG 343

RESULT 2  
CF672979  
LOCUS  
DEFINITION  
CF672979 541 bp mRNA linear EST 07-OCT-2003  
RTCNT1\_75\_F01\_A029 Root control Pinus taeda cDNA clone  
CF672979  
EST.  
pinus taeda (loblolly pine)  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus;  
1 (bases 1 to 541)  
Dean,J.F.D.  
Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Zimmermann,C. and  
An EST database from untreated loblolly pine (Pinus taeda) roots  
Unpublished (2003)  
Other ESTs: RTCNT1\_75\_F01.g1\_A029  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBR) and the CCLONES project a the

University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: M13-21 (TGTAACACGACGGCCAGT)  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1. .541  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="3 CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTCNT1\_75\_F01\_A029"  
/lab\_host="DH10B-Ti phage-resistant E. coli"  
/clone\_lib="Root control"  
/note="Organ: root; Vector: pSL1180; Site\_1: EcoRI; Site\_2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Just before harvesting roots for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 85.8%; Score 115.8; DB 14; Length 541;  
Best Local Similarity 91.1%; Pred. No. 4.7e-27;  
Matches 123; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 CTTGATTACGAGGTGATACGGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGACT 60  
|||||  
Db 66 CTTGATTACGAGGGGATACGGCTGCTACCAGCGGACAGGGCCCCGTGGAGAAGACT 125  
  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
|||  
Db 126 TCGTGTATATCTTGTATATGAAAGACAATCCTGGAACAACAGAGGAAGATGCTCTCAAT 185  
  
QY 121 CATATCAACGCCATG 135  
|||  
Db 186 CATCTCAACGCCATG 200

RESULT 3  
CF476978  
LOCUS  
DEFINITION  
CF476978 637 bp mRNA linear EST 08-SEP-2003  
RTMW3\_5\_A06.b1\_A022 Well-watered loblolly pine roots WW3 Pinus taeda cDNA clone RTMW3\_5\_A06\_A022 3', mRNA sequence.  
CF476978  
EST.  
Pinus taeda (loblolly pine)  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus;  
1 (bases 1 to 637)  
Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.  
An EST database from well-watered loblolly pine (Pinus taeda) roots  
Unpublished (2003)  
Other ESTs: RTMW3\_5\_A06.g1\_A022  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

TITLE  
JOURNAL  
COMMENT



/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTW3\_5\_A06\_A022"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WM3"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 85.8%; Score 115.8; DB 14; Length 745;  
Best Local Similarity 91.1%; Pred. No. 5.5e-27;  
Matches 123; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGGGTGCTACAGGGCGGACAGGGCTCGTGGAGAAGAAGCT 60  
|||||  
Db 461 CTTTCGATTACGAGGAGATACGGCTGCTACCGGGCGGACAGGGCCCGTGGAGAAGAAGCT 520  
|||||

QY 61 TCCTCTATATCATGTATATGAAAGACAATCCTCGAGTATCAGAGGAAGATGCTCTCGAT 120  
|||||

Db 521 TCGTGATATCTTGTATATGAAAGACAATCCTGGAGCAACGGAGAAGATGCTCTCAAT 580  
|||||

QY 121 CATATCAACGCCATG 135  
|||||

Db 581 CATATCAACGCCATG 595  
|||||

RESULT 6  
BX677624  
LOCUS  
DEFINITION BX677624 RN Pinus pinaster cDNA clone RN42B08, mRNA sequence.  
ACCESSION BX677624  
VERSION BX677624.1 GI:38011576  
KEYWORDS EST.  
SOURCE Pinus pinaster  
ORGANISM Pinus pinaster  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
1 (bases 1 to 517)  
Frigerio, J. and Plomion, C.  
Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach  
Unpublished (2002)  
Contact: Frigerio JM  
Genetique et Amelioration 69  
INRA  
route d'Arcachon 33612 Cestas CEDEX France  
Email: Frigerio@pierroton.inra.fr  
Email: Frigerio@pierroton.inra.fr  
Seq primer: T3.  
Location/Qualifiers  
1. .517  
/organism="Pinus pinaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:71647"  
/clone="RN42B08"  
/tissue\_type="root"  
/dev\_stage="6 weeks old seedling"  
/lab\_host="SOLR"  
/clone\_lib="RN"  
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN

Query Match 82.8%; Score 111.8; DB 12; Length 599;  
Best Local Similarity 88.1%; Pred. No. 1e-25;

Query Match 83.4%; Score 112.6; DB 13; Length 517;  
Best Local Similarity 89.6%; Pred. No. 5.2e-26;  
Matches 121; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGGGTGCTACAGGGCGGACAGGGCTCGTGGAGAAGAAGCT 60  
|||||  
Db 345 CTTTCGATTACGAGGGGACACTCGCTGCTACCGGGCGGACAGGGCCCGTGGAGAAGAAGCT 404  
|||||

QY 61 TCCTCTATATCATGTATATGAAAGACAATCCTCGAGTATCAGAGGAAGATGCTCTCGAT 120  
|||||

Db 405 TCGGTATATCTTGTATATGAAAGACAATCCTGGAACAACAGAGGAAGATGCTCTCAAT 464  
|||||

QY 121 CATATCAACGCCATG 135  
|||||

Db 465 CATATCAACGCCATG 479  
|||||

RESULT 7  
BG526917  
LOCUS  
DEFINITION BG526917 NXPV\_057\_D04\_F NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda cDNA clone NXPV\_057\_D04\_5' similar to Arabidopsis thaliana sequence At4g16730 limonene cyclase like protein see http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.  
ACCESSION BG526917  
VERSION BG526917.1 GI:13536796  
KEYWORDS EST.  
SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
1 (bases 1 to 599)  
Sederoff, R.  
Molecular Basis of Wood Formation in the Pine Megagenome  
Unpublished (2000)  
Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh, NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron.sederoff@ncsu.edu, jerrijohnson@ncsu.edu  
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further information.  
Seq primer: T3.  
Location/Qualifiers  
1. .599  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXPV\_057\_D04"  
/tissue\_type="Xylem"  
/cell\_type="Planings (secondary)"  
/dev\_stage="Transitional"  
/lab\_host="XL1-Blue"  
/clone\_lib="NXPV (Nsf Xylem Planings wood Vertical)"  
/note="Vector: Bluescript SK; Site\_1: Eco RI; Site\_2: XhoI; The library is from early (spring) secondary wood, taken from a ten year old tree in the transitional phase. The tree is a kind gift of the Westvaco Corporation. Secondary xylem was harvested from the tree by peeling back the bark and primary xylem and then removing the underlying tissue with a block plane. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCAGAG'."

FEATURES  
source

ORIGIN

Query Match 82.8%; Score 111.8; DB 12; Length 599;  
Best Local Similarity 88.1%; Pred. No. 1e-25;







ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
REFERENCE 1 (bases 1 to 542)  
AUTHORS Sederoff,R.  
TITLE Molecular Basis of Wood Formation in the Pine Megagenome  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh, NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron.sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further information.

Seq primer: T3.  
Location/Qualifiers  
1..542  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXSI\_099\_H06"  
/tissue\_type="xylem"  
/cell\_type="Side"  
/dev\_stage="Juvenile"  
/lab\_host="XL1-Blue"  
/clone\_lib="NXSI (Nsf Xylem Side wood Inclined)"  
/note="Vector: Bluescript SK; Site\_1: Eco RI; Site\_2: XhoI; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form side wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the sides of the inclined stems, and a mixture of all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI Bluescript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCAGG'."

ORIGIN  
Query Match 71.6%; Score 96.6; DB 10; Length 542;  
Best Local Similarity 82.2%; Pred. No. 9.5e-21;  
Matches 111; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 CTTGATTACGAGGTGATACGGGTGCTACAGCGGACAGGGCTCGTGGAGAAGAGCT 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 90 CTTGACTGAAAGGTGACACTCAATGCTACAGGCTGACAGGGCGCTGGAGAAGAGCT 149  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 150 TCGGCCGTATCGTGTATATGAAAGACCATCCTTGGATAACAGAGGAAGATGCTGTCAAT 209  
QY 121 CATATCAACGCCATG 135  
|| ||||| |||||  
Db 210 CAAGTCAATGCTATG 224

RESULT 11  
AW065088  
LOCUS  
DEFINITION ST39E04 Pine Triplex shoot tip library Pinus taeda cDNA clone  
ST39E04, mRNA sequence.  
ACCESSION AW065088  
VERSION AW065088.1 GI:6020160  
KEYWORDS EST.  
SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 574)  
AUTHORS Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.  
TITLE The Pine Gene Discovery Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Ross Whetten  
Forest Biotechnology Group  
North Carolina State University  
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh,NC, 27695-8008  
Tel: 919-515-7800  
Fax: 919-515-7801  
Email: rosswhet@unity.ncsu.edu  
Seq primer: 5' lambda Triplex2 Sequencing Primer.  
Location/Qualifiers  
1..574  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/db\_xref="taxon:3352"  
/clone="ST39E04"  
/lab\_host="E. coli BM25.8"  
/clone\_lib="Pine Triplex shoot tip library"  
/note="Organ: shoot tips; Vector: Lambda Triplex; Site\_1: SfiI (A); Site\_2: SfiI (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda Triplex vector. Plasmid subclones in pTriplex were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."

ORIGIN  
Query Match 71.6%; Score 96.6; DB 9; Length 574;  
Best Local Similarity 82.2%; Pred. No. 9.7e-21;  
Matches 111; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 CTTGATTACGAGGTGATACGGGTGCTACAGCGGACAGGGCTCGTGGAGAAGAGCT 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 23 CTTGACTGAAAGGTGACACTCAATGCTACAGGGCTGACAGGGCGCTGGAGAAGAGCT 82  
QY 61 TCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 83 TCGGCCGTATCGTGTATATGAAAGACCATCCTTGGATAACAGAGGAAGATGCTGTCAAT 142  
QY 121 CATATCAACGCCATG 135  
|| ||||| |||||  
Db 143 CAAGTCAATGCTATG 157

RESULT 12  
CF474640  
LOCUS  
DEFINITION RTWW2\_7\_B11.b1\_A021 Well-watered loblolly pine roots WW2 Pinus taeda cDNA clone RTWW2\_7\_B11\_A021 3', mRNA sequence.  
CF474640  
CF474640.1 GI:34492012  
EST.  
SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
REFERENCE 1 (bases 1 to 574)  
AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.  
An EST database from well-watered loblolly pine (Pinus taeda) roots  
Unpublished (2003)  
Other ESTs: RTWW2\_7\_B11.g1\_A021  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210

Email: mmpratt@uga.edu  
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: M13-21 (TGTAACACGACGGCCAGT)  
POLYA=Yes.

FEATURES  
source  
1. .574  
Location/Qualifiers  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTWW2\_7\_B11\_A021"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WW2"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN  
Query Match 71.6%; Score 96.6; DB 14; Length 574;  
Best Local Similarity 82.2%; Pred. No. 9.7e-21;  
Matches 111; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGGGTGCTACAAGCGGACAGGGCTCGTGAGAAGCT 60  
||||| |  
Db 50 CTTTCGACTGAAAGGTGACACTCAATGCTACAAGGCTGACAGGGCGCTGGAGAAGCT 109  
QY 61 TCCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
|| |  
Db 110 TCGGCCGTATCGTGTATATGAAGACCCTCTGGAATAACAGAGGAAGATGCTGTCAAT 169  
QY 121 CATATCAACGCCATG 135  
|| ||||| |||  
Db 170 CAAGTCAATGCTATG 184

RESULT 13  
CF479884/c  
LOCUS  
DEFINITION  
RTWW3\_12\_D02.g1\_A022 Well-watered loblolly pine roots WW3 Pinus taeda cDNA clone RTWW3\_12\_D02\_A022 5', mRNA sequence.  
CF479884  
CF479884.1 GI:34508753  
EST.  
Pinus taeda (loblolly pine)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J., Cannon,R., Owen,A. and Neale,D.  
EST database from well-watered loblolly pine (Pinus taeda) roots  
Other\_ESTs: RTWW3\_12\_D02.b1\_A022  
Unpublished (2003)  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the

University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: JENREV (CAGGAACAGCTATGACC).  
Location/Qualifiers  
1. .651  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTWW3\_12\_D02\_A022"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WW3"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

FEATURES  
source

ORIGIN

Query Match 71.6%; Score 96.6; DB 14; Length 651;  
Best Local Similarity 82.2%; Pred. No. 1e-20;  
Matches 111; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 CTTTCGATTACGAGGTGATACGGGTGCTACAAGCGGACAGGGCTCGTGAGAAGCT 60  
||||| |  
Db 461 CTTTCGACTGAAAGGTGACACTCAATGCTACAAGGCTGACAGGGCGCTGGAGAAGCT 402  
QY 61 TCCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTCGAT 120  
|| |  
Db 401 TCGGCCGTATCGTGTATATGAAGACCCTCTGGAATAACAGAGGAAGATGCTGTCAAT 342  
QY 121 CATATCAACGCCATG 135  
|| ||||| |||  
Db 341 CAAGTCAATGCTATG 327

RESULT 14  
CF401916

LOCUS  
DEFINITION  
CF401916 696 bp mRNA linear EST 29-AUG-2003  
RTWW1\_15\_B05.g1\_A015 Well-watered loblolly pine roots WW1 Pinus taeda cDNA clone RTWW1\_15\_B05\_A015 5', mRNA sequence.  
CF401916  
CF401916.1 GI:34360333  
EST.  
Pinus taeda (loblolly pine)

ORGANISM  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.  
REFERENCE  
AUTHORS  
An EST database from well-watered loblolly pine (Pinus taeda) roots  
Unpublished (2003)  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

TITLE  
JOURNAL  
COMMENT  
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2004, 09:55:09 ; Search time 8428.74 Seconds  
(without alignments)  
10351.438 Million cell updates/sec

Title: US-10-025-145A-64  
Perfect score: 2013  
Sequence: 1 ttttgacgtgccttcttctatc.....aaaaaaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2013	100.0	2013	6	AR222136	AR222136 Sequence
2	2013	100.0	2013	8	AGU87910	U87910 Abies grand
3	1306.8	64.9	2018	6	BD227661	BD227661 Synthases
4	1306.8	64.9	2018	6	AR222097	AR222097 Sequence
5	1306.8	64.9	2018	6	AR240696	AR240696 Sequence
6	1306.8	64.9	2018	6	AR266971	AR266971 Sequence
7	1306.8	64.9	2018	6	AR316320	AR316320 Sequence
8	1306.8	64.9	2018	6	AR338463	AR338463 Sequence
9	1306.8	64.9	2018	6	AR429869	AR429869 Sequence
10	1306.8	64.9	2018	8	AGU87909	U87909 Abies grand
11	1273.6	63.3	1958	8	AY237645	AY237645 Picea sit
12	1178.4	58.5	2082	8	AF543527	AF543527 Pinus tae
13	1155.6	57.4	2162	8	AF543529	AF543529 Pinus tae
14	1103.2	54.8	2186	8	AF461460	AF461460 Picea abi
15	1101.4	54.7	2198	8	AF369918	AF369918 Picea abi
16	1095.4	54.4	1893	8	AF139206	AF139206 Abies gra
17	1092.4	54.3	1890	6	AR222146	AR222146 Sequence
18	1085.8	53.9	2150	8	AF369919	AF369919 Picea abi
19	1072.4	53.3	2186	6	AR222137	AR222137 Sequence
20	1072.4	53.3	2186	8	AF139205	AF139205 Abies gra
21	1071.6	53.2	2196	6	BD227666	BD227666 Synthases
22	1071.6	53.2	2196	6	AR222096	AR222096 Sequence
23	1071.6	53.2	2196	6	AR240701	AR240701 Sequence
24	1071.6	53.2	2196	6	AR266976	AR266976 Sequence
25	1071.6	53.2	2196	6	AR316325	AR316325 Sequence
26	1071.6	53.2	2196	6	AR338468	AR338468 Sequence
27	1071.6	53.2	2196	6	AR429874	AR429874 Sequence
28	1071.6	53.2	2196	8	AGU87908	U87908 Abies grand
29	1071.6	53.2	2205	6	AR222116	AR222116 Sequence
30	1040.2	51.7	2100	8	AF543530	AF543530 Pinus tae
31	971.4	48.3	1960	8	AF543531	AF543531 Pinus tae
32	929.4	46.2	2429	6	AR222138	AR222138 Sequence
33	929.4	46.2	2429	8	AF139207	AF139207 Abies gra
34	925.4	46.0	2089	6	BD227677	BD227677 Synthases
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ALIGNMENTS

RESULT 1  
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LOCUS AR222136 2013 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 64 from patent US 6429014.  
ACCESSION AR222136  
VERSION AR222136.1 GI:23329510  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2013)  
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.  
TITLE Monoterpene synthases from grand fir (Abies grandis)  
JOURNAL Patent: US 6429014-A 64 06-AUG-2002;  
FEATURES Location/Qualifiers



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Query Match	100.0%;	Score 2013;	DB 6;	Length 2013;	
Best Local Similarity	100.0%;	Pred. No. 0;			
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QY	121	CAACTCTTGGAACTGACAGGCGGGGAAATCCGTCGCGCATTCCTATAAACATGTGTTGA	180		
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QY	241	GGGACGATGATTTCATACAGTCTCTGATCTCAACGCGCTTATGGAGCACCTGATTACCGGG	300		
Db	241	GGGACGATGATTTCATACAGTCTCTGATCTCAACGCGCTTATGGAGCACCTGATTACCGGG	300		
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QY	421	GAATCGACAGGCAATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAAACAGTTATT	480		
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QY	481	GGAAACGAAAAAGGCAATTGGATGTGGAGGGAGAGTGTGTGACTGACCTCAACTCAACCG	540		
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QY	541	CCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGTTTGAACG	600		
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QY	841	TGCCACGCTTGGAAAGCAAGGAATTACATGGACGTCCTTTGGACAGCACACTAAAAATAAGA	900		
Db	841	TGCCACGCTTGGAAAGCAAGGAATTACATGGACGTCCTTTGGACAGCACACTAAAAATAAGA	900		
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RESULT 2
AGU87910      2013 bp      mRNA      linear      PLN 10-AUG-2001
LOCUS          Abies grandis (-)-camphene synthase (AG6.5) mRNA, complete cds.
DEFINITION    U87910
ACCESSION     U87910
VERSION       U87910.1 GI:2411484
KEYWORDS
SOURCE
ORGANISM      Abies grandis
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              Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
REFERENCE     1 (bases 1 to 2013)
AUTHORS      Bohlmann,J., Steele,C.L. and Croteau,R.
TITLE        Monoterpene synthases from grand fir (Abies grandis). cDNA
              isolation, characterization, and functional expression of myrcene
              synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene
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JOURNAL       J. Biol. Chem. 272 (35), 21784-21792 (1997)
MEDLINE       97413772
PUBMED        9268308
REFERENCE     2 (bases 1 to 2013)
AUTHORS      Bohlmann,J., Phillips,M., Ramachandiran,V., Katoh,S. and Croteau,R.
TITLE        cDNA cloning, characterization, and functional expression of four
              new monoterpene synthase members of the Tpsd gene family from grand
              fir (Abies grandis)
JOURNAL       Arch. Biochem. Biophys. 368 (2), 232-243 (1999)
MEDLINE       99373092
PUBMED        10441373
REFERENCE     3 (bases 1 to 2013)
AUTHORS      Bohlmann,J., Steele,C.L. and Croteau,R.
TITLE        Direct Submission
JOURNAL       Submitted (31-JAN-1997) Institute of Biological Chemistry,
              Washington State University, Clark Hall, Pullman, WA 99164-6340,
              USA

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RESULT 3  
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LOCUS BD227661 2018 bp DNA linear PAT 17-JUL-2003  
DEFINITION Syntheses.  
ACCESSION BD227661  
VERSION BD227661.1 GI:33037431  
KEYWORDS JP 2002526066-A/13.  
SOURCE Abies grandis  
ORGANISM Abies grandis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Syntheses  
JOURNAL Patent: JP 2002526066-A 13 20-AUG-2002;  
UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR

BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES  
OS Abies grandis (giant fir)  
PN JP 2002526066-A/13  
PD 20-AUG-2002  
PF 17-SEP-1999 JP 2000574228  
PR 18-SEP-1998 US 60/100993,22-APR-1999 US 60/130628 PR  
23-AUG-1999 US 60/150262  
PI JOSEPH CHAPPELL, KATHLEEN R MANNA, JOSEPH P NOEL, COURTNEY M PI STARKS  
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Best Local Similarity 81.0%; Pred. No. 0;  
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AR222097  
LOCUS AR222097 2018 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 3 from patent US 6429014.  
ACCESSION AR222097  
VERSION AR222097.1 GI:23329471  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.  
TITLE Monoterpene synthases from grand fir (*Abies grandis*)  
JOURNAL Patent: US 6429014-A 3 06-AUG-2002;  
FEATURES Location/Qualifiers  
source 1. .2018  
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Query Match 64.9%; Score 1306.8; DB 6; Length 2018;  
Best Local Similarity 81.0%; Pred. No. 0;  
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;  
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RESULT 6

AR266971

LOCUS AR266971 2018 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 19 from patent US 6495354.

ACCESSION AR266971

VERSION AR266971.1 GI:29696426

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2018)

AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.

TITLE Syntheses

JOURNAL Patent: US 6495354-A 19 17-DEC-2002;

FEATURES

source location/Qualifiers

1..2018

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ORIGIN

Query Match 64.9%; Score 1306.8; DB 6; Length 2018;

Best Local Similarity 81.0%; Pred. No. 0;

Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

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RESULT 8  
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LOCUS  
DEFINITION  
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VERSION  
KEYWORDS  
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TITLE

AR338463  
Sequence 19 from patent US 6569656.  
AR338463  
AR338463.1 GI:33725240

2018 bp  
DNA  
linear  
PAT 17-AUG-2003

Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 2018)  
Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
Synthases





LOCUS AR429869 2018 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 19 from patent US 6645762.  
ACCESSION AR429869  
VERSION AR429869.1 GI:40190267  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Syntheses  
JOURNAL Patent: US 6645762-A 19 11-NOV-2003;  
FEATURES Location/Qualifiers  
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Query Match 64.9%; Score 1306.8; DB 6; Length 2018;  
Best Local Similarity 81.0%; Pred. No. 0;  
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QY 68 CAGGTCGTGCCTCAGTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT 127  
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ACCESSION U87909  
VERSION U87909.1 GI:2411482

Abies grandis  
Abies grandis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.

1 (bases 1 to 2018)  
Bohlmann,J., Steele,C.L. and Croteau,R.  
Monoterpene synthases from grand fir (Abies grandis): cDNA  
isolation, characterization, and functional expression of myrcene  
synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene  
synthase

J. Biol. Chem. 272 (35), 21784-21792 (1997)  
97413772  
9268308  
2 (bases 1 to 2018)  
Bohlmann,J., Steele,C.L. and Croteau,R.  
Direct Submission  
Submitted (31-JAN-1997) Institute of Biological Chemistry,  
Washington State University, Clark Hall, Pullman, WA 99164-6340,  
USA

FEATURES  
source Location/Qualifiers  
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AF543529  
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Pinus taeda (loblolly pine)  
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Phillips, M.A., Wildung, M.R., Williams, D.C., Hyatt, D.C. and  
Croteau, R.  
cDNA isolation, functional expression, and characterization of



JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL		(+)-alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine (Pinus taeda): Stereocontrol in pinene biosynthesis Arch. Biochem. Biophys. 411 (2), 267-276 (2003) 22510022 12623076 2 (bases 1 to 2162) Phillips,M.A., Wildung,M.R., Williams,D.C. and Croteau,R.B. Direct Submission Submitted (09-SEP-2002) Institute of Biological Chemistry, Washington State University, PO Box 646340, Pullman, WA 99164-6340, USA	
FEATURES	source	Location/Qualifiers 1..2162 /organism="Pinus taeda" /mol_type="mRNA" /db_xref="taxon:3352" 59..1942 /note="monoterpene synthase; Pt10" /codon_start=1 /product="alpha-terpineol synthase" /protein_id="AA061227.1" /db_xref="GI:28894486"	
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QY	141	CCGGGGAATCCGTCCGCGCATTCCTCCATAAACATGTGTTTGACAAGCGTCGCATCTACTGAT	200
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AF461460			
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DEFINITION	Picea abies (+)-3-carene synthase (JF67) mRNA, complete cds.		
ACCESSION	AF461460		
VERSION	AF461460.1	GI:29293033	
KEYWORDS			
SOURCE	Picea abies (Norway spruce)		
ORGANISM	Picea abies		
REFERENCE			
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.		
	Faeldt,J., Martin,D., Miller,B., Rawat,S. and Bohlmann,J.		
	Traumatic resin defense in Norway spruce (Picea abies): methyl		
	jasmonate-induced terpene synthase gene expression, and cDNA		
	cloning and functional characterization of (+)-3-carene synthase		
JOURNAL	Plant Mol. Biol. 51 (1), 119-133 (2003)		
MEDLINE	22490501		
PUBMED	12602896		
REFERENCE	2 (bases 1 to 2186)		
AUTHORS	Faeldt,J. and Bohlmann,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-DEC-2001) Biotechnology Laboratory, University of		
	British Columbia, 237-6174 University Blvd, Vancouver, BC V6T1Z4,		
	Canada		
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	POLNFI RHRHVEFYTLVSGIDMEPKHCTFRLSFKMCHLITVLDDMYDTFGTIDELRL		
	FTAAVKRWDPSTTECLPEYMKGVYTVLYETVNEMAEQAKSQGRDRTL SVRQALEAYI		
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	KFNDFACSLRLRGDTRCYQADRARGEAEASCISCYMKDNPGSTQEDALNHNNMIET		
	IKLNLWELLKPDNNVPISSKKHAFDINRGLHFFYNYRDGYTVASNETKNLVIKTVLEP		

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QY	124	CTCTTGGAATCTGCAGGCCGGGAAATCCGTCGCGCATTTCCATAAACAATGTGTTTGACAA	183		
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QY	304	GTGCTGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAG	363		
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Db	917	AAAATCAAATGCTAGATGTGAACACCAAGAAAGTTTTTAGAACTTGCAAAATTGGAGTTCA	976		
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QY	766	TGCAAAAGATTCCGGCATCCAGTATACCTTCACTAGAGATACGGGACGTTCTGGAATATG	825
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1306.8	64.9	2018	4	AAF73372
5	1092.4	54.3	1890	4	AAF73421
6	1072.4	53.3	2186	4	AAF73412
7	1071.6	53.2	2196	2	AAX08643
8	1071.6	53.2	2196	3	AAA38927
9	1071.6	53.2	2196	4	AAF73371
10	1071.6	53.2	2205	2	AAX08663
11	1071.6	53.2	2205	4	AAF73391
12	929.4	46.2	2429	4	AAF73413
13	925.4	46.0	2089	2	AAX08645
14	925.4	46.0	2089	3	AAA38938
15	925.4	46.0	2089	4	AAF73373
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17	805.8	40.0	1634	3	AAA69644
18	623.6	31.0	1173	3	AAA69643
19	471	23.4	696	4	AAF73414
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29	427	21.2	2700	3	AAA38931	Aaa38931	Yew taxad
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39	390.2	19.4	1785	2	AAX87535	Aax87535	Gamma-hum
40	390.2	19.4	1785	3	AAA38934	Aaa38934	Grand fir
41	388.6	19.3	779	3	AAA69642	Aaa69642	Pinus rad
42	387.8	19.3	2525	2	AAX87530	Aax87530	E-alpha-b
43	333.6	16.6	2861	3	AAA38937	Aaa38937	Grand fir
44	285.8	14.2	462	3	AAA69611	Aaa69611	Pinus rad
45	267.2	13.3	1416	2	AAX08656	Aax08656	Grand Fir

ALIGNMENTS

RESULT 1  
AAF73411  
ID AAF73411 standard; cDNA; 2013 BP.  
XX  
AC AAF73411;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 64.  
XX  
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
XX  
DR WPI; 2001-182782/18.  
DR P-PSDB; AAB69390.  
XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
PS Claim 8; Page 147-149; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants

SQ	Sequence	2013 BP; 591 A; 432 C; 464 G; 526 T; 0 U; 0 Other;	
	Query Match	100.0%; Score 2013; DB 4; Length 2013;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2013; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	TTTTGACGTGCTTCTTATCTGATAGCAAGCTGAAATGGCTCTTCTTCTATTACTCCGC	60
Db	1	TTTTGACGTGCTTCTTATCTGATAGCAAGCTGAAATGGCTCTTCTTCTATTACTCCGC	60
QY	61	TGGTTTCCAGTTCGTGCTCAGTTCTTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCC	120
Db	61	TGGTTTCCAGTTCGTGCTCAGTTCTTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCC	120
QY	121	CAACTCTTTGGAATCTGCAGGCCGGGGAATCCGTGCGCATTCCTATAAACAATGTTGA	180
Db	121	CAACTCTTTGGAATCTGCAGGCCGGGGAATCCGTGCGCATTCCTATAAACAATGTTGA	180
QY	181	CAAGCGTCGCATCTACTGATTCTGTACAGAGACGCGTGGGCAACTATCATTTCCAACTGT	240
Db	181	CAAGCGTCGCATCTACTGATTCTGTACAGAGACGCGTGGGCAACTATCATTTCCAACTGT	240
QY	241	GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCTTATGGAGCACCTGATTACCGGG	300
Db	241	GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCTTATGGAGCACCTGATTACCGGG	300
QY	301	AACGTGCTGACAGACTTATTTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGG	360
Db	301	AACGTGCTGACAGACTTATTTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGG	360
QY	361	AAGATGGAGGCAATGATCTCCTTCAACGACTTTTGGTGGTCGATGACGTTGAAAGTTGG	420
Db	361	AAGATGGAGGCAATGATCTCCTTCAACGACTTTTGGTGGTCGATGACGTTGAAAGTTGG	420
QY	421	GAATCGACAGGCAATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAAACAGTTATT	480
Db	421	GAATCGACAGGCAATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAAACAGTTATT	480
QY	481	GGAACGAAAAAGGCATTTGGATGTGGGAGGAGAGTGTGTGACTGACCTCAACTCAACCG	540
Db	481	GGAACGAAAAAGGCATTTGGATGTGGGAGGAGAGTGTGTGACTGACCTCAACTCAACCG	540
QY	541	CCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGTTTGAACG	600
Db	541	CCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGTTTGAACG	600
QY	601	TTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCGCAATATTCAGATAGAGGAGAGA	660
Db	601	TTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCGCAATATTCAGATAGAGGAGAGA	660
QY	661	TTAGAGGCGTTCTCAATTTANTCAGGGCCTCCCTCGTCGCTTTCCCGCGGAGAAAGTTA	720
Db	661	TTAGAGGCGTTCTCAATTTANTCAGGGCCTCCCTCGTCGCTTTCCCGCGGAGAAAGTTA	720
QY	721	TGGATGAAGCTGAAACATTTCTCTACAAAAATATTTAAGAGAAGCCCTGCAAAAAGATTCCGG	780
Db	721	TGGATGAAGCTGAAACATTTCTCTACAAAAATATTTAAGAGAAGCCCTGCAAAAAGATTCCGG	780
QY	781	CATCCAGTATACTTTCACTAGAGATACGGGACGTTCTTGGAAATGTTGGCACACCAAT	840
Db	781	CATCCAGTATACTTTCACTAGAGATACGGGACGTTCTTGGAAATGTTGGCACACCAAT	840
QY	841	TGCCACGCTTGGAAAGCAAGGAATTACATGGACGCTTTTGGACAGCACACTAAAAATAAGA	900
Db	841	TGCCACGCTTGGAAAGCAAGGAATTACATGGACGCTTTTGGACAGCACACTAAAAATAAGA	900
QY	901	ACGCCGCGAGAAACTTTTAGAAGTTGCAAAATTTGGAATTCATATATTTCACTCCTTAC	960
Db	901	ACGCCGCGAGAAACTTTTAGAAGTTGCAAAATTTGGAATTCATATATTTCACTCCTTAC	960
QY	961	AAGAGAGAGAGTTAAAAACATGTTTCCCGATGGTGGAAAGACTCGGGTTCTCCTGAGATGA	1020
Db	961	AAGAGAGAGAGTTAAAAACATGTTTCCCGATGGTGGAAAGACTCGGGTTCTCCTGAGATGA	1020

QY	1021	CCTTCTGTCGACATCGTCACGTGGAATACTACGTTTGGCTTCTGCAATTCGTTTCGAGC	1080
Db	1021	CCTTCTGTCGACATCGTCACGTGGAATACTACGTTTGGCTTCTGCAATTCGTTTCGAGC	1080
QY	1081	CTCAACATTTCTGGATTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCACGGTTCCTG	1140
Db	1081	CTCAACATTTCTGGATTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCACGGTTCCTG	1140
QY	1141	ACGACATGTACGACGCTTTCGGCACAGTAGACGAGCTGGAACCTTTCACAGCGACAATTA	1200
Db	1141	ACGACATGTACGACGCTTTCGGCACAGTAGACGAGCTGGAACCTTTCACAGCGACAATTA	1200
QY	1201	AGAGATGGGATCCGTCCGCGATGGAATGCGCTTCCAGAATAATGAAAGGAGTGTACATGA	1260
Db	1201	AGAGATGGGATCCGTCCGCGATGGAATGCGCTTCCAGAATAATGAAAGGAGTGTACATGA	1260
QY	1261	TGGTTTATCACACCCGTAATGAAATGGCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACA	1320
Db	1261	TGGTTTATCACACCCGTAATGAAATGGCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACA	1320
QY	1321	CGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTTTGATTTCGTATATGAGGAAAGCAA	1380
Db	1321	CGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTTTGATTTCGTATATGAGGAAAGCAA	1380
QY	1381	AGTGGATCGCCACTGGTTATCTGCCCCACGTTTGGAGGAGTACTTGGAGAACGGGAAAGTTA	1440
Db	1381	AGTGGATCGCCACTGGTTATCTGCCCCACGTTTGGAGGAGTACTTGGAGAACGGGAAAGTTA	1440
QY	1441	GCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTTGGACATCCCTTTCCTG	1500
Db	1441	GCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTTGGACATCCCTTTCCTG	1500
QY	1501	ATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGTATATGTATCATCC	1560
Db	1501	ATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGTATATGTATCATCC	1560
QY	1561	TTGATTAAAGAGTGATACACGGTGCTACAAGGCAGACAGGGCCCCGTGGAGAGAAAGCTT	1620
Db	1561	TTGATTAAAGAGTGATACACGGTGCTACAAGGCAGACAGGGCCCCGTGGAGAGAAAGCTT	1620
QY	1621	CGTCTATATCATGTATATGAAAGACAAATCCTCGATTAAACGGAGAAAGATGCTCTGAATC	1680
Db	1621	CGTCTATATCATGTATATGAAAGACAAATCCTCGATTAAACGGAGAAAGATGCTCTGAATC	1680
QY	1681	ATATCAACTTTCATGATCAGGACGCAATCAGAGAAATTAATTTGGAGCTTCTTAAAGCCAG	1740
Db	1681	ATATCAACTTTCATGATCAGGACGCAATCAGAGAAATTAATTTGGAGCTTCTTAAAGCCAG	1740
QY	1741	ACAAACAGTGTCCCATCACTTCCAAGAAACACGCAATTAAGCAGAGTTTGGCATC	1800
Db	1741	ACAAACAGTGTCCCATCACTTCCAAGAAACACGCAATTAAGCAGAGTTTGGCATC	1800
QY	1801	ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAACAAAGAGTTTGGTGA	1860
Db	1801	ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAACAAAGAGTTTGGTGA	1860
QY	1861	TGAGAACCGTCATTTGAACCTGTGCTTGTGTAACAACACTCAATATTAATTAAGT	1920
Db	1861	TGAGAACCGTCATTTGAACCTGTGCTTGTGTAACAACACTCAATATTAATTAAGT	1920
QY	1921	AGGATGCCCTATGGGTGTATATAGGGCACACAAAAATAAATATGGTGTGTAGTAAAGC	1980
Db	1921	AGGATGCCCTATGGGTGTATATAGGGCACACAAAAATAAATATGGTGTGTAGTAAAGC	1980
QY	1981	TGTAATTTATGAAAAAATAAAAAAAAAAAAAA 2013	
Db	1981	TGTAATTTATGAAAAAATAAAAAAAAAAAAAA 2013	

RESULT 2

AAx08644

ID AAX08644 standard; cDNA; 2018 BP.











XX										
SQ	Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;									
	Query Match	64.9%; Score 1306.8; DB 4; Length 2018;								
	Best Local Similarity	81.0%; Pred. No. 0;								
	Matches 1595; Conservative	0;	Mismatches	342;	Indels	33;	Gaps	5;		
QY	68	CAGGTCGTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGACAATCCCAACTCT	127							
Db	53	CAAAATCGTTGATCAGTTCTACCCATGAGCTTAAGGCTCTCTCTAGACAATCCAGCTCT	112							
QY	128	TGGAATCTGCAGGCCGGGAAATCCGTGCGCATTCATATAACATGTGTTTGACAAGCGT	187							
Db	113	AGGAATGAGTAGCGGAGGGAATCTATCACTCTTCCATCAGCATGAGCTCTACCACCGT	172							
QY	188	CGCATCTACTGATTTGTACAGAGACGCGTGGGCAACTATCATTCCAAACCTGTGGACGA	247							
Db	173	TGTAACCGATGATGGTGTACGAAGACGCATGGCGATTTCCATTCCAACTCTGGGACGA	232							
QY	248	TGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGGAACGTGC	307							
Db	233	TGATGTCATACAGTCT---TTACCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGC	289							
QY	308	TGACAGACTTATTCGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG	367							
Db	290	TGAGAAACTGATCGGGGAAGTAAAG---AACATGTTCAATTCGATGTCATTAGAAGATGG	346							
QY	368	AG-----GCAATGATCTCCTTCAACGACTTTTGTGCTGGTCGATGACGTTGA	412							
Db	347	AGAGTTAATGAGTCGCTCAATGATCTCAATTCACGCTTTTGGATTGTCGACAGCCTTGA	406							
QY	413	ACGTTTGGGAATCGACAGGCATTTCAAAAAGAGATAAAAAACGGCACTCGATTATGTTAA	472							
Db	407	ACGTTTGGGATCCATAGACATTTCAAAGATGAGATAAAAATCGGCGCTTGATTATGTTTA	466							
QY	473	CAGTTATTGGAACGAAAAAGGCATTGGATGTGGGAGGGAGAGTGTGTGACTGACCTCAA	532							
Db	467	CAGTTATTGGGCGGAAAAATGGCATCGGATCGGGAGGGAGAGTGTGTTACTGATCTGAA	526							
QY	533	CTCAACCGCCTTGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT	592							
Db	527	CTCAACTGCGTTGGGCTTCGAACCTACGACTACACGGATACCCGGTGTCTTCAGATGT	586							
QY	593	TTTGAACGTTTTTAAAGACAAAAATGGCAATTTTCTCCAATGCTGCCAATATTCAGATAGA	652							
Db	587	TTTCAAAGCTTTCAAAGGCCAAAAATGGCAGTTTTTCTGCTCTGAAAATATTCAGACAGA	646							
QY	653	GGGAGAGATTAGAGGCGTTCTCAATTTATTACGGGCTCCCTCGTCGCTTTCCCGGCGA	712							
Db	647	TGAAGAGATCAGAGGCGTTCTGAATTTATTCCGGGCTCCCTCATTTGCCCTTTCCAGGGGA	706							
QY	713	GAAAGTTATGGATGAAGCTGAAACATTTCTCTACAAAATATTAAAGAGAAGCCCTGCAAAA	772							
Db	707	GAAAATTATGGATGAGGCTGAAATCTTCTCTACCAAAATATTAAAGAGAAGCCCTGCAAAA	766							
QY	773	GATTCGGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA	832							
Db	767	GATTCGGTCTCCAGT---CTTTCGGAGAGATCGGGGACGTTTGGAAATATGTTGGCA	823							
QY	833	CACCAATTTGCCACGCTTGAAGCAAGGAATTACATGGACGCTCTTTGGACAGCACACTAA	892							
Db	824	CACATATTTGCCCGGATTTGAAGCAAGGAATTACATCCAAGTCTTTGGACAGGACACTGA	883							
QY	893	AAATAAGAACGC-----CGCCGAGAAACTTTTAGAACTTGCAAAATTTGGAATTCAA	943							
Db	884	GAACACGAAGTCATA TGTGAAGAGCAAAAACTTTTAGAACTCGCAAAATTTGGAGTTCAA	943							
QY	944	TATATTTCACTCTTACAAGAGAGAGAGTTAAAAACATGTTTCCCGATGGTGGAAAGACTC	1003							
Db	944	CATCTTTCAATCTTTACAAAAGAGGGAGTTAGAAAAGTCTGGTCAGATGGTGGAAAGAATC	1003							
QY	1004	GGGTTCTCCTGAGATGACCTTCTGTGACATCGTCACGTGGAATACTACGCTTTGGCTTC	1063							

Db	1004	GGGTTTTCCTGAGATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTGGCTTC	1063
QY	1064	CTGCATTGCGTTGAGCCCTCAACATTTCTGGATTTCAGACTCGGCTTTTACCAAGATGTCTCA	1123
Db	1064	CTGCATTGCGTTGAGCCCTCAACATTTCTGGATTTCAGACTCGGCTTTGCCAAGACGTGTCA	1123
QY	1124	TCTTATCAGGTTCTTTGACGACATGTACGACGTCTTCCGCCACAGTAGACGAGCTGGAAT	1183
Db	1124	TCTTATCAGGTTCTTTGACGATATGTACGACACTTCCGCCACAGTAGACGAGCTGGAAT	1183
QY	1184	CTTCACAGCGACAATTAAGAGATGGGATCCGTCCGCGATGGAATGCCTTCCAGAATATAT	1243
Db	1184	CTTCACAGCGACAATGAAGAGATGGGATCCGTCCGTATAGATTGCTTCCAGAATATAT	1243
QY	1244	GAAAGGAGTGTACATGATGTTTATCACACCGTAAATGAAATGGTCCGAGTGGCAGAGAA	1303
Db	1244	GAAAGGAGTGTACATAGCGGTTTACGACACCGTAAATGAAATGGTCCGAGAGGAGAGGA	1303
QY	1304	GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTGTTGATTTC	1363
Db	1304	GGCTCAAGGCCGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATGATTTC	1363
QY	1364	GTATATGCAAGAAAGCAAGTGGATCGCCACTGGTTATCTGCCCCACGTTTGAGGAGTACTT	1423
Db	1364	GTATATGCAAGAAAGCAAGTGGATCGCCACTGGTTACCTGCCCCCTCTTTGATGAGTACTA	1423
QY	1424	GGAGAACGGGAAAGTTAGTCTCTGCTCATCGCCCATGCGCACTGCCAATCTCTGACGTT	1483
Db	1424	CGAGAAATGGGAAAGTTAGTCTGTGTCATCGCATATCCGCATTTGCAACCCATCTTGACAAT	1483
QY	1484	GGACATCCCTTTCTCTGATCACATCCTCAAGAAAGTTGACTTCCCATCGAAGCTCAATGA	1543
Db	1484	GGACATCCCTTTCTCTGATCATATCCTCAAGAAAGTTGACTTCCCATCAAGCTTAAACGA	1543
QY	1544	CTTGATATGTATCATCCTTCGATTAAAGAGGTGATACACAGGTGCTACAGGACAGACAGGC	1603
Db	1544	CTTGGCATGTGCCATCCTTCGATTACGAGGTGATACGCGGTGCTACAGGCGGACAGGC	1603
QY	1604	CCGTGGAGAAAGCTTCGTCTATATCATGTTTATGAAAGACAATCCTGGATTAAACGGA	1663
Db	1604	TCGTGGAGAAAGCTTCCTCTATATCATGTTTATGAAAGACAATCCTGGAGTATCAGA	1663
QY	1664	AGAAATGCTCTGATCATATCAACTTCATGATCAGGACGCAATCAGAGAAATTAATTTG	1723
Db	1664	GGAAGATGCTCTCGATCATATCAACGCCATGATCAGTACGTAATCAAAGGATTAAATTTG	1723
QY	1724	GGAGCTTCTAAAGCCAGACAACAGTGTTCCTATCACTTCCAAGAAAACACGCAATTTGACAT	1783
Db	1724	GGAACCTTCTCAAAACCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACAT	1783
QY	1784	AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA	1843
Db	1784	CGCCAGAGCTTTCCATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA	1843
QY	1844	AACAAAAGAGTTTGGTGTAGAGAACCGTCAATGAAACCTGTGCTTGTAAACAACACTTCAA	1903
Db	1844	AACGAAGAGTTTGGTCAAGAGAACCTCCTTGAATCTGTGCTTGTAGCAACAGCTCAA	1903
QY	1904	ATCTACAATATTAACTGAGGATGCCCTATGGGTGTATATAGGGCACACAAAAATAATAT	1963
Db	1904	ATCTATGCCCTATGCTATGTCGGGTTAAATATATATGGAAGGTAGCCGTTGGATGTAGA	1963
QY	1964	GGTGTGTTAGTAAAGCTGTAAATTTATGAAAAAATAAAAAAAAAAAAAA 2013	
Db	1964	GGATAAGTTTGTATTAAATTAAGTTGTAATTTAAAAAATAAAAAAAAAA 2013	

RESULT 5  
AAF73421  
ID AAF73421 standard; cdna; 1890 BP.  
XX  
AC AAF73421;  
XX

DT	30-APR-2001	(first entry)
XX		
DE	Grand fir monoterpene synthase coding sequence	SEQ ID NO: 77.
XX		
KW	Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;	
KW	myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;	
KW	terpinolene synthase; insect resistance; nutrition; ss.	
XX		
OS	Abies grandis.	
XX		
PN	WO200107565-A2.	
XX		
PD	01-FEB-2001.	
XX		
PF	24-JUL-2000; 2000WO-US020264.	
XX		
PR	26-JUL-1999; 99US-00360545.	
XX		
PA	(UNIW ) UNIV WASHINGTON STATE RES FOUND.	
XX		
PI	Steele CL, Bohlmann J, Croteau RB, Phillips MA;	
XX		
DR	WPI; 2001-182782/18.	
DR	P-PSDB; AAB69393.	
XX		
PT	New nucleic acid encoding monoterpene synthases, for increasing terpene	
PT	synthesis in plants, e.g. for increasing resistance to pests or for	
PT	treatment of cancer.	
XX		
PS	Claim 18; Page 163-165; 175pp; English.	
XX		
CC	The present invention provides the protein and coding sequences of	
CC	monoterpene synthases from the grand fir. These include (-)-camphene	
CC	synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-	
CC	limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase	
CC	and pinene synthase. The sequences can be used to produce transgenic	
CC	plants expressing high levels of the enzymes, resulting in levels which	
CC	are useful in protecting against and treating cancers, and to confer	
CC	insect resistance on plants	
XX		
SQ	Sequence 1890 BP; 550 A; 381 C; 441 G; 518 T; 0 U; 0 Other;	
	Query Match	54.3%; Score 1092.4; DB 4; Length 1890;
	Best Local Similarity	76.8%; Pred. No. 3.6e-299;
	Matches 1439; Conservative	0; Mismatches 396; Indels 39; Gaps 7
QY	46	TTTCTATTACTCCGCTGTTTCCAGGTCGTGCCTCAGTTCCTCTCATGAGATTAGGCTC 105
Db	26	TGTCCTCCAAATCGGTCTCTGCACAAATCGTGGATCGTTTCTACTATGAGCATAAGGCTA 85
QY	106	TCCGTAGAACAAATCCCAACTCTTGGAACTCTGCAGGCCGGGGAATCCGTCGGCATTCOA 165
Db	86	TCAGTAGAACAAATCCCAATCTTGGATTGCTGGCGAGGGAATCTGTGACACATTCCC 145
QY	166	TAAACATGTGTTTGACAAAGCGTCGCATCTACTG---ATTCTGTACAGACGCGTGGCA 222
Db	146	TGAGAAATGAGTTTGAGCACCGCAGTCTCTGATGATCATGGTGTAAGACGCATAGTCG 205
QY	223	ACTATCATTTCCAAACCTGTGGACGATGATTTCATACAGTCTCTGATCTCAACGCCTTATG 282
Db	206	AGTTTTCATTCCAATCTGTGGACGACGATTTCATACAATCTC---TATCAACGCCTTATG 262
QY	283	GAGCACCTGATTACCGGGAACGCTGTGACAGACTTATTGGGGAAGTAAAGGATATAATGT 342
Db	263	GGGCACCTTCATACCGTGAACGCTGTGATAGACTTATTGTGGAAGTAAAGGTATA---T 319
QY	343	TCAATTTCAAGTCGCTGGAAGATGGAG-----GCATGATCTCCTTCAAC 387
Db	320	TCACTTCAATTTCAGCGGAAGATGGAGAACTAATCACTCCCTCAATGATCTCATTCAAC 379
QY	388	GACTTTTGTGTCGATGACGTTGAAACGTTTGGGAATCGACAGGCAATTTCAAAAAAGAGA 447
Db	380	GCCTTTTAATGGTCGATAACGTTGAACGTTTAGGGATTGATAGACATTTCAAAAAATGAGA 439







Db 1038 GGGTTTGCTGAACCTGACCTTTGGTCGGCATCGTCAGTGGAACTACTACACCCTGAGCTC 1097  
QY 1064 CTGCATTGCGTTCGAGCCTCAACATTTCTGGATTCGACTCGGCTTTACCAAGATGTCTCA 1123  
Db 1098 TTGCATTGCGACTGAGCCCAACATTTCTGCATTCGATTTGGCTTTGCCAAACGTTGTC 1157  
QY 1124 TCTTATCACGGTTCCTGACGACATGTACGACGTCTTCGGCACAGTAGACGAGCTGGAAC 1183  
Db 1158 TCTTATCACGGTTCCTGACGATATCTACGACATTTTCGGAACGATGGATGAAATCGAAC 1217  
QY 1184 CTTTACAGCGCAATTAAGAGATGGGATCCGTCGCGGATGGAATGCCCTTCACAGATATAT 1243  
Db 1218 CTTCAACGAGGCAGTTAGGAGATGGAATCCGTCGGAGAAAGAACGCCCTCCCAGATATAT 1277  
QY 1244 GAAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA 1303  
Db 1278 GAAAGAAATCTACATGGCACTCTACGAAGCCTTAACTGACATGGCGGAGAGGACAGAGAA 1337  
QY 1304 GGCTCAAGGCCGAGACAGCTCAACTATGCAAGACAGGCTTTGGGAGCGTGTGTTTGATTC 1363  
Db 1338 GACACAAGGCCGAGACAGCTCAATTATGCTAGAAAGGCTTTGGGAAGTTTATCTTGATTC 1397  
QY 1364 GTATATGCAGGAAGCAAAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAGGAGTACTT 1423  
Db 1398 GTATACACAAGCAAGCAAAAGTGGATCGCCAGCGGTATCTGCCAACTTTTCGAGGAGTACTT 1457  
QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCCATCGCCACTGCAACCCATTTCTGACGTT 1483  
Db 1458 AGAGAACGCGAAGGTTAGCTCTGGTCTATCGTGCAGCGGCATTGACACCCCTCTGACATT 1517  
QY 1484 GGACATCCCTTTCTGTATCATACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543  
Db 1518 GGACGTACCGCTTCCGTATGACGTCTTGAAGGGAATAGATTTTCCATCGAGATTAATGA 1577  
QY 1544 CTTGATATGTATCATCCTTCGATTAAAGAGGTGATACACGGTGCTACAAGGCACAGGGC 1603  
Db 1578 TTTGGCATCTTCCTTCCTTAGACTAAGAGGTGACACACGATGCTACAAGGCACAGGGA 1637  
QY 1604 CCGTGGAGAAGAAGCTTCGCTATATCATGTATTATGAAAAGACAATCCTGGATTAAACGGA 1663  
Db 1638 CCGAGGAGAAGAAGCGTCAAGCATATCGTGTACATGAAAGACAATCCCGGATTAAACAGA 1697  
QY 1664 AGAAGATGCTCTGATCATATCAACTTTCATGATCAGGGACGCAATCAGAGAAATTAAATTG 1723  
Db 1698 GGAAGATGCTCTCAATCATATCAATGCGCATGATCAACGACATAATCAAGAAATTAATTG 1757  
QY 1724 GGAGCTTCTAAAGCCAGACAAACAGTGTTCCTCCATCACTTCCAAGAAACACGCAATTTGACAT 1783  
Db 1758 GGAACCTTCTCAAACCCGATAGCAATATTCCAATGACTGCACGGAAACATGCTTATGAGAT 1817  
QY 1784 AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843  
Db 1818 AACCAGAGCTTTCACCAACTTTACAAATATAGAGATGGCTTCAGCGTTGCCACTCAAGA 1877  
QY 1844 AACAAAGAGTTTGGTGATGAGAAACCGTCAATTGAACCTGTGCCCTTTGTAAACAACACTTCAA 1903  
Db 1878 AACGAAAAGTTTGGTGAGGAGAACGGTCCCTTGAACCAAGTGCCTCTTTAAACAATTTAAACC 1937  
QY 1904 ATCTACAATA 1913  
Db 1938 TTCTATAATA 1947

RESULT 7

AAAX08643  
ID AAAX08643 standard; cDNA; 2196 BP.

XX AC  
AAAX08643;

XX  
DT 27-SEP-1999 (first entry)

XX DE  
Myrcene synthase gene.

XX  
KW Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.  
XX  
OS Abies grandis.  
XX  
FH Key Location/Qualifiers  
FT CDS 69..1952  
FT /\*tag= a  
FT /product= "Myrcene synthase"  
XX  
PN WO9902030-A1.  
XX  
XX 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014528.  
XX  
PR 11-JUL-1997; 97US-0052249P.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Bohlmann J, Steele CL, Croteau RB;  
XX  
DR WPI; 1999-120396/10.  
DR P-PSDB; AAW85700.  
XX  
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. myrcene, limonene or pinene.  
XX  
PS Claim 9; Page 69-72; 121pp; English.  
XX  
CC Nucleotide sequences encoding myrcene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by myrcene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal  
XX  
SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Query Match 53.2%; Score 1071.6; DB 2; Length 2196;

Best Local Similarity 75.0%; Pred. No. 3.1e-293;

Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGGTCGTGCCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCCCAACTCT 127  
Db 116 CAAGTCGTTGATCAGTTCAATTTCATGAACATAAGCCTCCCTATAGAACAAATCCCAATCT 175  
QY 128 TGAATCTGCAGCGCGGGAATCCGTCGGCATTCATAAACATGTGTTTGACAAAGCGT 187  
Db 176 TGAATCGGTAGCGGAGGAAATCTGTACGCTTCCATGAGCATCAGTTTGGCCACCGC 235  
QY 188 CGCATCTACTGATTTGTACAGAGACGCGTGGCAACTATCATTCCAACCTGTGGGACGA 247  
Db 236 TGCACCTGATGGTGTACAAAGACGCATAGGTGACTACCATTCCAATATCTGGGACGA 295  
QY 248 TGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATACCGGGAACGTGC 307  
Db 296 TGATTTTCATACAGTCTC---TATCAACGCCCTTATGGGAACCCCTCTTACCAGGAACGTGC 352  
QY 308 TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTTCAATTTCAAGTCGCTGGAAGATGG 367  
Db 353 TGAGAGATTAAATTGTGGAGGTTAAAGAGATA---TTCAATTTCAATGTACTCTGGATGATGG 409  
QY 368 AGG-----CAATGATCTCCTCAACGACTTTTGTGGTCGATGACGTTGA 412  
Db 410 AAGATTAAATGAGTTCCCTTTAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGA 469

QY 413 ACGTTTGGGAATCGACAGGCATTCTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAA 472  
|||||  
Db 470 ACGTTTGGGATAGCTAGACATTCTCAAGAACGAGATAACATCAGCTCTGGATTATGTTT 529  
|||||  
QY 473 CAGTTATTGGAACGAAAAAGGCATTGGATGTGGAGGGAGAGTGTGTGACTGACCTCAA 532  
|||||  
Db 530 CCGTTACTGGGAGAAAAACGGCATTTGGATGTGGAGAGACAGTATTGTTACTGATCTCAA 589  
|||||  
QY 533 CTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT 592  
|||||  
Db 590 CTCAACTCGCTTGGGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT 649  
|||||  
QY 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTCTCCACTGCCAATATTACAGATAGA 652  
|||||  
Db 650 TTTAAAAGCTTTTCAAGATCAAAATGGACAGTTTGTATGCTCCCC---GGTCAGACAGA 706  
|||||  
QY 653 GGGAGAGATTAGAGCGTTCTCAATTTATTACGGCCCTCCCTCGTCGCCCTTCCCGCGCA 712  
|||||  
Db 707 GGGTGAGATCAGAAAGCTTCTTAACCTTATATCGGGCTTCCCTCATTTGCCCTTCCCTGGTGA 766  
|||||  
QY 713 GAAAGTTAAGGATGAAGCTGAAACATTTCTCTACAAAAATATTTAAGAGAAGCCCTGCAAAA 772  
|||||  
Db 767 GAAAGTTATGGAAGAAGCTGAAATCTTCTCCACAAGATATTTGAAAAGAGCTCTACAAAA 826  
|||||  
QY 773 GATTCGGCATCCAGTATACCTTTCACTAGAGATAACGGGACGTTCTGGAATATGGTTGGCA 832  
|||||  
Db 827 GATTCAGTCTCCGCT--CTTTCAACAAGAGATAAAGTTTGTATGGAATATGGCTGGCA 883  
|||||  
QY 833 CACCAATTTGCCACGCTTGAAGCAAGGAATTTACATGGACGCTCTTTGGACAGCACACTA- 891  
|||||  
Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTTACATAGACACACTTGAGAAAAGACACCAG 943  
|||||  
QY 892 -----AAATAAAGACGCCGCCGAGAAAATTTTAGAACTTGCAAAAATTTGGAATTCAA 943  
|||||  
Db 944 TGCATGGCTCAATAAATAATGCTGGGAAGAAGCTTTTAGAACTTGCAAAATTTGAGATTCAA 1003  
|||||  
QY 944 TATATTTCACTCCTTACAAGAGAGAGAGTTAAACAATGTTTCCCAGATGGTGAAGACTC 1003  
|||||  
Db 1004 TATATTTAACTCCTTACAACAAAAAGGAATTTACAATATCTTTTGAGATGGTGAAGAGTC 1063  
|||||  
QY 1004 GGGTTCTCCTGAGATGACCTTCTGTGACATCGTCACGTGGAATACTACGCTTGGCTTC 1063  
|||||  
Db 1064 GGATTTGCCTAAATTGACATTTGCTCGGCATCGTCATGTGGAATTTCTACACTTTGGCCTC 1123  
|||||  
QY 1064 CTGCATTCGGTTCGAGCCTCAACATTTCTGGATTCAGACTCGGCTTTTACCAAGATGTCTCA 1123  
|||||  
Db 1124 TTGTATTGCCATTGACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCA 1183  
|||||  
QY 1124 TCTTATCACGGTTCTTGACGACATGTACGACGCTCTTCGGCACAGTAGACGAGCTGGAAC 1183  
|||||  
Db 1184 TCTTGTACAGTTTTTGGACGATATTTACGACACTTTTGGAACGATTGACGAGCTTGAAC 1243  
|||||  
QY 1184 CTTACAGCGACAATTAAGAGATGGGATCCGTCGCCGATGGAATGCCCTTCCAGATATAT 1243  
|||||  
Db 1244 CTTACATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGATATAT 1303  
|||||  
QY 1244 GAAAGGAGTGACATGATGGTTTATCACACCGTTAAATGGAATGGCTCGAGTGGCAGAGAA 1303  
|||||  
Db 1304 GAAATGTGTGTACATGCTCGTGTGTTTGAACCTGTAATGAACCTGACACGAGAGCGGAGAA 1363  
|||||  
QY 1304 GGCTCAAGCGCGAGACACGCTCAACTATGCAAGACGGCTTGGAGGGCGTGTGTTGATTC 1363  
|||||  
Db 1364 GACTCAAGGGAGAAAACACTCTCAACTATGTTTCGAAAAGCTTGGAGGCTTATTTGATTC 1423  
|||||  
QY 1364 GTATATGCAGGAAGCAAAAGTGATCGCCACTGTTTATCTGCCACGTTTGAGGAGTACTT 1423  
|||||  
Db 1424 ATATATGGAAGAAGCAAAATGGATCTTAATGGTTATCTGCCAATGTTTGAAGAGTACCA 1483  
|||||  
QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCCACTTCTGACGTT 1483  
|||||  
Db 1484 TGAGAAATGGAAAGTGAGCTCTGCATATCGCGTAGCAACATTTGCAACCCCACTCTCACCTT 1543  
|||||  
QY 1484 GGACATCCCCCTTTCTCTGATCACATCTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543  
|||||

Db 1544 GAATGCATGGCTTCCTGATTACATCTTGAAGGAATTGATTTCCATCCAGGTTCAATGA 1603  
|||||  
QY 1544 CTTGATATGTATCATCTCTTCGATTAAAGAGGTGATACACGGTGTCTACAAGCAGACAGGC 1603  
|||||  
Db 1604 TTTGGCATCGTCTCTTCGGCTACGAGGTGACACACGGTGTCTACAAGCCGATAGGA 1663  
|||||  
QY 1604 CCGTGGAGAGAAGCTTCGTCTATATCATGTATATGAAAGACAATCCTCGATTAAACGA 1663  
|||||  
Db 1664 TCGTGGTGAAGAAGCTTCGTGTATATCATGTTATATGAAAGACAATCCTGGATCAACCGA 1723  
|||||  
QY 1664 AGAAGATGCTCTGAATCATATCAACTTTCATGATCAGGGACGCAATCAGAGAAATTAATTG 1723  
|||||  
Db 1724 AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATAATCAAGAAATTAATTG 1783  
|||||  
QY 1724 GGAGCTTCTAAAGCCAGACAAACAGTGTTCCTCATCACTTCCAAGAAAACACGCAATTTGACAT 1783  
|||||  
Db 1784 GGAACCTTCTAAGATCCAACGACAATATTCCAATGCTGGCCAAGAAACATGCTTTTGACAT 1843  
|||||  
QY 1784 AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGTACAGCTTTGCCAACGTTGA 1843  
|||||  
Db 1844 AACAAGAGCTCTCCACCATCTCTACATATATCAGATGGCTTTAGTGTGCCAACAAAGGA 1903  
|||||  
QY 1844 AACAAAGAGTTTGTGATGAGAACCGTCAATGCAACCTGTGCCTTTGTAAACAACACTTCAA 1903  
|||||  
Db 1904 AACAAAAAAATTTGTTATGGAACACACTCTTGAATCTATGCTTTTAACTATAACCATA 1963  
|||||  
QY 1904 ATCTACAATATTAACTGAGGATGCCCTATGGGTGTATATAGGGCACA 1950  
|||||  
Db 1964 TCCATAATAATAAGCTCATAATGCTAAATTTATTTGGCCTTATGACATA 2010  
|||||

RESULT 8

AAA38927  
ID AAA38927 standard; DNA; 2196 BP.

AAA38927;

25-AUG-2000 (first entry)

Grand fir myrcene synthase DNA sequence SEQ ID NO:29.

Synthase; protein co-ordinate data; active site; modification; terpenoid;  
3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;  
isoprenoid; breeding programme; fragrance; flavour; pheromone;  
defensive agent; pigment; antitumour; steroid hormone;  
signal transduction pathway; bile acid; affinity purification;  
photoreceptor; enzymatic synthesis; nutrient supplement;  
immunological reagent; ds.

Abies grandis.

WO200017327-A2.

30-MAR-2000.

17-SEP-1999; 99WO-US021419.

18-SEP-1998; 98US-0100993P.

22-APR-1999; 99US-0130628P.

23-AUG-1999; 99US-0150262P.

(KENT ) UNIV KENTUCKY RES DEPT.

(SALK ) SALK INST BIOLOGICAL STUDIES.

Chappell J, Manna KR, Noel JP, Starks CM;

WPI; 2000-292839/25.

P-PSDB; AAY90842.

Novel terpene synthase enzymes, useful for producing terpene  
hydrocarbons, e.g. fragrances or antitumor agents, are derived from known  
enzymes by specific amino acid alterations.

The present invention describes an isolated terpene synthase (I) comprising a region with at least 20% identity to region 265-535 of a 548 amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha-carbon atoms (alphaC) that have interatomic distances, between each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom ) within tabulated ranges, and have an ordered arrangement of R groups (defining aa side chains), excluding specific tabulated arrangements (tables given in the specification). (I), and related enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, antitumour agents, components of signal transduction pathways, precursors of steroid hormones and bile acids, as photoreceptors and as co-factor side chains. Some synthases with little or no catalytic activity (and nucleic acids encoding them) are used as controls in the analysis of products formed by enzymatic synthesis; as nutrient supplements; for affinity purification of isoprenoids; or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthase or inheritance of the gene in plant breeding programs. The new synthases may produce novel terpene products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent sequences used in the exemplification of the present invention

Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Query Match	53.2%;	Score 1071.6;	DB 3;	Length 2196;
Best Local Similarity	75.0%;	Pred. No. 3.1e-293;		
Matches 1430;	Conservative 0;	Mismatches 441;	Indels 36;	Gaps 6;
Qy 68	CAGGTCGTGCCTCAGTCTTCTCTCATGAGATTAAGGCTCTCCGATAGAACAAATCCCAACTCT	127		
Db 116	CAAGTCGTTGATCAGTTCATTAATTCATGAACATAAGCCTCCCTATAGAACAAATCCCAATCT	175		
Qy 128	TGGAATCTGCAGCGCGGAAATCCGTGCGCATTCATATAAATCATGTGTTTGACAAGCGT	187		
Db 176	TGGAATCGGTAGCGGAGGAAATCTGTACGCCTTCCATGAGCATCAGTTGGCCACCGC	235		
Qy 188	CGCATCTACTGATTCTGTACAGAGACGCGTGGGCAACTATCATTTCCAACCTGTGGGACGA	247		
Db 236	TGCACCTGATGATGGTGTACAAAGACGCATAGGTGACTACCATTCCAATATCTGGGACGA	295		
Qy 248	TGATTTCATACAGTCTCTGATCTCAACGCCTTATGGAGCACTGATTACCGGGAACGTGC	307		
Db 296	TGATTTTCATACAGTCTC---TATCAACGCCTTATGGGGAACCCCTCTTACCAGGAACGTGC	352		
Qy 308	TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG	367		
Db 353	TGAGAGATTAAATTGTGGAGTAAAGAAGATA---TTCAATTCAATGTACCTGGATGATGG	409		
Qy 368	AGG-----CAATGATCTCCTTCAACGACTTTTGTGCTGATGACGTTGA	412		
Db 410	AAGATTAAATGAGTTCCTTTAATGATCTCATGCAACGCCTTTGGATAGTCGATAGCGTTGA	469		
Qy 413	ACGTTTGGGAATCGACAGGCATTTCAAAAAGAGATAAAAACGGCACTCGATTATGTTAA	472		
Db 470	ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTT	529		
Qy 473	CAGTTATTGGAACGAAAAGGCATTTGGATGTGGGAGGGAGAGTGTGTGACTGACCTCAA	532		
Db 530	CCGTTACTGGGAGGAAAACGGCATTTGGATGTGGGAGAGACAGTATTGTTACTGATCTCAA	589		
Qy 533	CTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT	592		
Db 590	CTCAACTGCGTTGGGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT	649		
Qy 593	TTTGAACGTTTTTTAAAGACAAAAAATGGCAATTTTCTCCACTGCCAATATTTCAGATAGA	652		
Db 650	TTTAAAAGCTTTTCAAGATCAAAAATGGACAGTTTGTATGCTCCCC---GGTCAGACAGA	706		
Qy 653	GGGAGAGATTAGAGCGGTTCTCAATTTATTTCAGGGCCTCCCTCGTCGCTTTTCCCGCGGA	712		



QY	1784	AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA	1844
Db	1844	AACAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGGCCAACAAGGA	1903
QY	1844	AACAAAGAGTTTGGTGATGAGAACCGTCAATTGAACCTGTGCCTTTGTAAACAACACTTCAA	1903
Db	1904	AACAAAAAATTGGTTATGGAAACACTCCTTGAATCTATGCTTTTAACTATAAACCATA	1963
QY	1904	ATCTACAATATTAACTGAGGATGCCCTATGGGTGTATATAGGGCACA	1950
Db	1964	TCCATAATAATAAGCTCATAATGCTAAATTATTGGCCTTATGACATA	2010
RESULT 9			
AAAF73371			
ID	AAAF73371 standard; cDNA; 2196 BP.		
XX			
AC	AAAF73371;		
XX			
DT	30-APR-2001 (first entry)		
XX			
DE	Grand fir myrcene synthase coding sequence SEQ ID NO: 1.		
XX			
KW	Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;		
KW	myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;		
KW	terpinolene synthase; insect resistance; nutrition; ss.		
XX			
OS	Abies grandis.		
XX			
PN	WO200107565-A2.		
XX			
PD	01-FEB-2001.		
XX			
PF	24-JUL-2000; 2000WO-US020264.		
XX			
PR	26-JUL-1999; 99US-00360545.		
XX			
PA	(UNIW ) UNIV WASHINGTON STATE RES FOUND.		
XX			
PI	Steele CL, Bohlmann J, Croteu RB, Phillips MA;		
XX			
DR	WPI; 2001-182782/18.		
DR	P-PSDB; AAB69370.		
XX			
PT	New nucleic acid encoding monoterpene synthases, for increasing terpene		
PT	synthesis in plants, e.g. for increasing resistance to pests or for		
PT	treatment of cancer.		
XX			
PS	Claim 28; Page 103-106; 175pp; English.		
XX			
CC	The present invention provides the protein and coding sequences of		
CC	monoterpene synthases from the grand fir. These include (-)-camphene		
CC	synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-		
CC	limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase		
CC	and pinene synthase. The sequences can be used to produce transgenic		
CC	plants expressing high levels of the enzymes, resulting in levels which		
CC	are useful in protecting against and treating cancers, and to confer		
CC	insect resistance on plants		
XX			
SQ	Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;		
Query Match 53.2%; Score 1071.6; DB 4; Length 2196;			
Best Local Similarity 75.0%; Pred. No. 3.1e-293;			
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;			
QY	68	CAGGTCGTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT	127
Db	116	CAAGTCGTTGATCAGTTCAATTATGAACATAAAGCCTCCCTATAGAACAAATCCCAATCT	175
QY	128	TGGAATCTGCAGGCCGGGAAATCCGTCGCGCAATCCATAAACATGTGTTGACAAGCGT	187
Db	176	TGGAATGCGTAGCGGAGGAAATCTGTACGCCCTCCATGAGCATCAGTTTGGCCACCGC	235

QY	188	CGCATCTACTGATTCTGTACAGAGACGCGTGGGAAACTATCATTTCCAAACCTGTGGACGA	247
Db	236	TGCACCTGATGATGGTGTACAAAGACGCATAGTGACTACCATTTCCAATATCTGGGACGA	295
QY	248	TGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGAAACGTGC	307
Db	296	TGATTTTCATACAGTCTC---TATCAACGCCCTTATGGGAAACCCCTCTTACAGGAAACGTGC	352
QY	308	TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG	367
Db	353	TGAGAGATTAAATTGGAGGGTAAAGAAGATA--TTCAATTTCAATGTACCTGGATGATGG	409
QY	368	AGG-----CAATGATCTCCTTCAACGACTTTTGTGCTGCTCGATGACGTTGA	412
Db	410	AAGATTAAATGAGTTCCTTTAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGA	469
QY	413	ACGTTTGGGAATCGACAGGCATTTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAA	472
Db	470	ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTT	529
QY	473	CAGTTATTGGAAACGAAAAAGGCATTGGATGTGGAGGGGAGAGAGTGTGTGACTGACCTCAA	532
Db	530	CCGTTACTGGGAGGAAAAACGGCATTTGGATGTGGAGAGACAGATTGTGTTACTGATCTCAA	589
QY	533	CTCAACCGCCTTTGGGCTTCGAACCTCTCCGACTACACGGATACACTGTGTCTTCAGATGT	592
Db	590	CTCAACTCGGTTGGGCTTTCGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT	649
QY	593	TTTGAACGTTTTTAAAGACAAAAAATGGCAATTTTCTCCACTGCCAATATTCAGATAGA	652
Db	650	TTTAAAAAGCTTTTCAAGATCAAAAATGGACGTTTGTATGCTCCCCC---GGTCAGACAGA	706
QY	653	GGGAGAGATTAGAGCGCTTCTCAATTTAATTCAGGGCCTCCCTCGTCGCCCTTTCCCGGCGA	712
Db	707	GGGTGAGATCAGAAGCGTTCCTTAACCTTATATCGGGCTTCCCTCATTTGCCCTTCCCTGGTGA	766
QY	713	GAAAGTTATGGATGAAGCTGAAACATTTCTCTCAAAAAATATTTAAGAGAAAGCCCTGCAAAA	772
Db	767	GAAAGTTATGGAAGAGCTGAAATCTTCTCCACAAGATATTTTGAAAGAAGCTCTACAAA	826
QY	773	GATTCGGGCATCCAGTATACCTTTCACTAGAGATACGGGACGTTCTCGGAATATGGTTGGCA	832
Db	827	GATTCAGTCTCCGCT---CTTTCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCA	883
QY	833	CACCAATTTGCCACGCTTGGAAAGCAAGGAATTACATGGACGCTTTTGGACAGCACACTA-	891
Db	884	CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAG	943
QY	892	-----AAAATAAGAAACGCCCGCAGAAAACTTTTAGAACCTTGCAAAATTTGGAATTCAA	943
Db	944	TGCATGGCTCAATAAAAAATGCTGGGAAGAAAGCTTTTAGAACCTTGCAAAATTTGGAGTTCAA	1003
QY	944	TATATTTCACTCCTTACAAGAGAGAGAGTAAACCATGTTTCCCGATGGTGGAAAGACTC	1003
Db	1004	TATATTTAACTCCTTACAACAAAGGAATTACAATATCTTTTGAGATGGTGGAAAGAGTC	1063
QY	1004	GGGTTCTCCTGAGATGACCTTCTGTGACACATCGTCACGTGGAATACACGCTTTGGCTTC	1063
Db	1064	GGATTTGCCCTAAATTGACATTTTGCTCGGCATCGTCATGTGGAATTCACACTTTGGCCTC	1123
QY	1064	CTGCATTTGGGTTTCGAGCCTCAACATTTCTGGATTCAGACTCGGCTTTACCAAGATGTCTCA	1123
Db	1124	TTGTATTGCCATTCACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCA	1183
QY	1124	TCTTATCACGGTTCTTGACGACATGTACGACGCTCTTCGGCACAGTAGACGCTGGAAC	1183
Db	1184	TCTTGTCAACAGTTTGGACGATATTTACGACACTTTTGGAAACGATTGACGAGCTTGAAC	1243
QY	1184	CTTCACAGCGACAATTAAAGAGATGGGATCCGTCGCCGATGGAATGCCCTCCAGAATATAT	1243
Db	1244	CTTCACATCTGCAATTAAAGAGATGGAATTTCATCAGAGATAGAACACCTTCAGAAATATAT	1303





Db 638 TTTAAAGCTTTTCAAGATCAAAATGGACAGTTTGTATGCTCCCC---GGTCAGACAGA 694

QY 653 GGGAGAGATTAGAGGGTTCTCAATTTATTACGGGCTCCCTCGTCGCCCTTCCCGCGA 712

Db 695 GGGTGAGATCAGAAAGCGTCTTAACTTATATCGGGCTCCCTCATTTGCTTCCCTGGTGA 754

QY 713 GAAAGTTATGGATGAAGCTGAAACATTTCTCTACAAAATATTTAAGAGAAGCCCTGCAAAA 772

Db 755 GAAAGTTATGGAAGAGCTGAAATCTTCTCCACAGATATTTGAAAGAAGCTTACAAA 814

QY 773 GATTCCGGCATCCAGTATACTTTTCACTAGAGATACGGGACGTTCTGGAATATGGTTGGCA 832

Db 815 GATTCCAGTCTCCGCT---CTTTCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCA 871

QY 833 CACCAATTTGCCACCGTTGGAAGCAAGGAATTACATGGACGCTCTTTGGACAGCACACTA- 891

Db 872 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAG 931

QY 892 -----AAATAAAGACGCCCGCGAGAACTTTTAGAACTTGCAAAATTTGAATTCAA 943

Db 932 TGCATGGCTCAATAAAATGCTGGGAAGAGCTTTTAGAACTTGCAAAATTTGAGATTCAA 991

QY 944 TATATTTCACTCCTTACAAGAGAGAGAGTTAAACATGTTTCCCGAUGGTGGAAGACTC 1003

Db 992 TATATTTAACTCCTTACAACAAAAGGAATTACATATCTTTTGAGATGGTGGAAAGAGTC 1051

QY 1004 GGGTCTCTCTGAGATGACCTTCTGTGACATCGTCACGTGGAATACTACGCTTTGGCTTC 1063

Db 1052 GGATTTGCCCTAAATTGACATTTGCTCGGCATCGTCATGTGGAATTTCTACACITTTGCCCTC 1111

QY 1064 CTGCATTGCGTTTCGAGCCTCAACATTTCTGGAATTCAGACTCGGCTTTTACCAGATGTCCTCA 1123

Db 1112 TTGTATTGCCATTGACCCAAAACATTTCTGCATTAGACTAGGCTTCGCCAAAATGTGTCA 1171

QY 1124 TCTTATCACGGTTCTTGACGACATGTACGACGCTTTCGGCACAGTAGACGAGCTGGAAC 1183

Db 1172 TCTTGTCAACAGTTTTCGACGATATTTACGACACTTTTGGAAACGATTGACGAGCTTGAAC 1231

QY 1184 CTTTACAGCGACAAATTAAGAGATGGGATCCGTCGCGCATGGAATGCCTTCCAGAAATATAT 1243

Db 1232 CTTTCAATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACTTCCAGAAATATAT 1291

QY 1244 GAAAGGAGTGTACATGATGGTTTATCACACCCGTAATGAAATGGCTCGAGTGGCAGAGAA 1303

Db 1292 GAAATGTGTACATGGTTCGTGTTTGAAACTGTAAATGAACTGACACGAGAGCGGAGAA 1351

QY 1304 GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTGTTGATTC 1363

Db 1352 GACTCAAGGGAGAAACACTCTCAACTATGTTTCAAAGGCTTGGGAGGCTTATTTGATTC 1411

QY 1364 GTATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCACGTTTGGAGAGTACTT 1423

Db 1412 ATATATGGAAGAAGCAAAATGGATCTCTAATGGTTATCTGCCAACGTTTGAAGAGTACCA 1471

QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTTCTGACGTT 1483

Db 1472 TGAGAAATGGGAAAGTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCTCACTTT 1531

QY 1484 GGACATCCCTTTCTGATCATCATCTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543

Db 1532 GAATGCATGGCTTCTGATTACATCTTGAAGGGAATTGATTTTCCATCCAGGTTCAATGA 1591

QY 1544 CTTGATATGTATCATCTCTTCGATTAAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGCG 1603

Db 1592 TTTGGCATCGTCTCTCTTCGGCTACGAGGTGACACACGCTGTCTACAAGGCCGATAGGGA 1651

QY 1604 CCGTGAGAGAAGCTTCGTCTATATCATGTTATATGAAAGACAATCTCGAATTAACGGA 1663

Db 1652 TCGTGGTGAAGAAGCTTCGTGTATATCATGTTATATGAAAGACAATCTCTGGATCAACCGA 1711

QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGAGAAATTAATTTG 1723

Db 1712 AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATAATCAAAAGAAATTAATTTG 1771

QY 1724 GGAGCTTCTAAAGCCAGACAAACAGTGTTCCTCATCTTCCAAGAAACACGCATTTGACAT 1783

Db 1772 GGAACCTTCTAAGATCCAAACGACAATATTTCCAATGCTGGCCAAGAAACATGCTTTTGACAT 1831

QY 1784 AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843

Db 1832 AACAAAGAGCTCTCCACCATCTCTACATATATCAGATGGCTTTAGTGTTCACCAAGGA 1891

QY 1844 AACAAAAGAGTTTGGTGATGAGAACCGTCAATTGAACCTGTGCCCTTTGTAAACAACACTTCAA 1903

Db 1892 AACAAAAAAATTGGTTATGGAACACACTCTCTGAATCTATGCTTTTTTAACATAAACCATATA 1951

QY 1904 ATCTACAATATTAACTGAGGATGCCCTATGGGTGTATATAGGGCACA 1950

Db 1952 TCCATAATAATAAGCTCATAATGCTAAATTTATTGGCCTTATGACATA 1998

RESULT 11

AAF73391

ID AAF73391 standard; cDNA; 2205 BP.

XX

AC AAF73391;

XX 30-APR-2001 (first entry)

XX Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 31.

DE Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;

XX myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;

KW terpinolene synthase; insect resistance; nutrition; ss.

KW Abies grandis.

XX WO200107565-A2.

PN 01-FEB-2001.

XX 24-JUL-2000; 2000WO-US020264.

PF 26-JUL-1999; 99US-00360545.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

PA Steele CL, Bohlmann J, Croteu RB, Phillips MA;

PI WPI; 2001-182782/18.

XX P-PSDB; AAB69380.

PT New nucleic acid encoding monoterpene synthases, for increasing terpene synthesis in plants, e.g. for increasing resistance to pests or for treatment of cancer.

XX Example 3; Page 135-137; 175pp; English.

XX The present invention provides the protein and coding sequences of monoterpene synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants

CC Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;

XX Query Match 53.2%; Score 1071.6; DB 4; Length 2205;

XX Best Local Similarity 75.0%; Pred. No. 3.1e-293;

XX Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGGTCGTGCTCAGTCTTCTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCCCAACTCT 127

Db 104 CAAGTCGTTGATCAGTTCATTAATTCATGAACATAAAGCTCCCTATAGAACAAATCCCAATCT 163

QY	128	TGGAATCTGCAGGCCGGGAAATCCGTCGGCATTCCATAAAACATGTTGTTGACAAAGCGT	187
Db	164	TGGAATGCGTAGCCGAGGAAATCTGTACGCCCTTCCATGAGCATCAGTTGGCCACC	223
QY	188	CGCATCTACTGATTCTGTACAGAGACCGGTGGGCAACTATCATTCCAACCTGTGGACGA	247
Db	224	TGCACCTGATGGTGTACAAAGACGCATAGGTGACTACCATTCCTCAATATCTGGACGA	283
QY	248	TGATTTCTACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTAACCGGAAACGTGC	307
Db	284	TGATTTCTACAGTCTC---TATCAACGCATTAATGGGAAACCTCTTACCAAGAAACGTGC	340
QY	308	TGACAGACTTATTTGGGGAAGTAAAGGATATAATGTTCAAATTCAGTCGCTGGAAGATGG	367
Db	341	TGAGAGATTAAATGTTGGAGGTAAAGAAGATA---TTCAAATTCATGTTACCTGGATGATGG	397
QY	368	AGG-----CAATGATCTCCTTCAACGACTTTTGTGCTGGTCGATGACGTTGA	412
Db	398	AAGATTAAATGAGTTCCTTTAATGATCTCATGCAACGCCTTTGGATAGTCGATAGCGTTGA	457
QY	413	ACGTTTGGGAATCGACAGGCATTTCAAATAAGAGATAAAAAACGGCACCTCGATTATGTTAA	472
Db	458	ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTT	517
QY	473	CAGTTATTGGAACGAAAGAGCATTTGGATGTGGGAGGAGAGTGTGTTGACTGACCTCAA	532
Db	518	CCGTTACTGGGAGGAAACGGCATTTGGATGTGGGAGAGACAGTATTGTTACTGATCTCAA	577
QY	533	CTCAACCGCCTTGGGCTTCGAACCTCTCCGACTACACGGATACACTGTGTCTTCAGATGT	592
Db	578	CTCAACTGCGTTGGGTTTCGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT	637
QY	593	TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATTTCAGATAGA	652
Db	638	TTTAAAGCTTTTCAAGATCAAAATGGACAGTTTGTATGTCCTCCCTC---GGTCAGACAGA	694
QY	653	GGGAGAGATTAGAGCGTTCCTCAATTTATTCAGGCGCTCCCTCGTCGCTTCCCGCGCA	712
Db	695	GGGTGAGATCAGAAGCGTCTTAACTTATATCGGGCTTCCCTCATTTGCCCTTCCCTGGTGA	754
QY	713	GAAAGTTATGGATGAAGCTGAAACATTTCTCTACAAAAATTTAAAGAGAAAGCCCTGCAAAA	772
Db	755	GAAAGTTATGGAAGAGCTGAAATCTTCTCCACAAGATATTGAAAGAAGCTCTACAAAA	814
QY	773	GATTCGGGCATCCAGTATATCTTCACTAGAGATACGGGACGTTCTTGAATATGTTGGCA	832
Db	815	GATTCAGTCTCCGCT---CTTTCAAGAGATAAAGTTTGTATGGAATATGGCTGGCA	871
QY	833	CACCAATTTGCCACGCTTGGAAGCAAGGAATTACATGGACGTTTGGACAGCACACTA-	891
Db	872	CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAG	931
QY	892	-----AAAAATAAGAACGCCGCGAGAAAACTTTTAGAACTTGCAAAATTTGGAATTCAA	943
Db	932	TGCATGGCTCAATAAAAAATGCTGGGAAGAAAGCTTTTAGAACTTGCAAAATTTGAGTTCAA	991
QY	944	TATATTTCACTCCTTACAAGAGAGAGAGTTAAAAACATGTTTCCGATGGTGGAAAGACTC	1003
Db	992	TATATTTAACTCCTTACAACAAAAGGAATTACAATATCTTTTGAGATGGTGGAAAGAGTC	1051
QY	1004	GGGTTCTCTGAGATGACCTTCTGTGACATCGTCACGTGGAATATCTACGCTTTGGCTTC	1063
Db	1052	GGATTTGCCATAAATTGACATTTGCTCGGCATCGTCATGTGGAATTTACACTTTGGCCTC	1111
QY	1064	CTGCAATGCGTTGAGCCCTCAACATTTCTGGAATTCAGACTCGGCTTTACCAAGATGTCCTCA	1123
Db	1112	TTGTATTGCCATTGACCCCAAAACATTCTGCAATTCAGACTAGGCTTCGCCCAAAATGTGTCA	1171
QY	1124	TCCTATACAGGTTCTTGACGACATGTACGACGCTCTTCGGCACAGTAGACGCTGGAAC	1183
Db	1172	TCCTGTACAGTTTGTGACGATATTTACGACACTTTTGGAAACGATTGACGAGCTTGAAC	1231

QY	1184	CTTCACAGCGACAATTAAGAGATGGGATCCGTCGGCATGGAATGCCTTCCAGATATAT	1243
Db	1232	CTTCACATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGATATAT	1291
QY	1244	GAAAGGAGTGTACATGATGTTTATCACACCCTAAATGAAATGGCTCGAGTGGCAGAGAA	1303
Db	1292	GAAATGTGTACATGTCGTCGTTTGAAACTGTAAATGAACTGACACGAGAGCGGAGAA	1351
QY	1304	GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACACGCTTGGGAGGCGTGTGTTGATTC	1363
Db	1352	GACTCAAGGGAGAAACACTCTCAACTATGTTTCGAAAGGCTTGGGAGGCTTATTTGATTC	1411
QY	1364	GTATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCCCACGTTTGAGGAGTACTT	1423
Db	1412	ATATATGGAAGAAGCAAAATGGATCTTAATGGTTATCTGCCAACGTTTGAAGAGTACCA	1471
QY	1424	GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCGCACTGCAACCCATTCTGACGTT	1483
Db	1472	TGAGAAATGGGAAAGTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCCTCACTTT	1531
QY	1484	GGACATCCCTTTCTCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA	1543
Db	1532	GAATGCATGGCTTCTCTGATTACATCTTGAAGGGAATTGATTTCCATCCAGGTTCAATGA	1591
QY	1544	CTTGATATGTATCATCCTTCGATTAAGAGGTGATACACGGTGTCTACAAAGGCAGACAGGGC	1603
Db	1592	TTTGGCATCGTCTTCTTCCGCTACGAGGTGACACACGCTGTCTACAAAGGCCGATAGGGA	1651
QY	1604	CCGTGGAGAAAGCTTCGTCTATATCATGTTATGAAAGACAATCCTGGATTAAACGGA	1663
Db	1652	TCGTGGTGAAGAAGCTTCGTGTATATCATGTTATGAAAGACAATCCTGGATCAACCGA	1711
QY	1664	AGAAGATGCTCTGAATCATATCAACTTCAATCATGATCAGGAGCGCAATCAGAGAATTAATTTG	1723
Db	1712	AGAAGATGCCCTCAATCATATCAATCAATGCTCAATGACATATCAAGAATTAATTTG	1771
QY	1724	GGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCACTTCCAAAGAAACACGCAATTTGACAT	1783
Db	1772	GGAACCTTCTAAGATCCAACGACATAATTCCAATGCTGGCCAAAGAAACATGCTTTTGACAT	1831
QY	1784	AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA	1843
Db	1832	AACAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACCAAGGA	1891
QY	1844	AACAAGAGTTTGGTGATGAGAACCGTCATTAACCTGTGCTTGTAAACAAACACTTCAA	1903
Db	1892	AACAAAAAATTTGGTTATGGAACACTCCTTGAATCTATGCTTTTAACTATAACCATA	1951
QY	1904	ATCTACAATATTAACTGAGGATGCCCTATGGGTGTATATAGGGCACA	1950
Db	1952	TCCATAATAAAGCTCATAATGCTAAATATTGGCCCTTATGACATA	1998

RESULT 12

AAF73413

ID AAF73413 standard; cDNA; 2429 BP.

XX

AC AAF73413;

XX

DT 30-APR-2001 (first entry)

XX

DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 68.

XX

KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;

KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;

KW terpinolene synthase



24-JUL-2000; 2000WO-US020264.  
26-JUL-1999; 99US-00360545.  
(UNIW ) UNIV WASHINGTON STATE RES FOUND.  
Steele CL, Bohlmann J, Croteau RB, Phillips MA;  
WPI; 2001-182782/18.  
P-PSDB; AAB69392.

New nucleic acid encoding monoterpene synthases, for increasing terpene synthesis in plants, e.g. for increasing resistance to pests or for treatment of cancer.

Claim 23; Page 156-159; 175pp; English.

The present invention provides the protein and coding sequences of monoterpene synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants

Sequence 2429 BP; 726 A; 484 C; 512 G; 707 T; 0 U; 0 Other;

Query Match 46.2%; Score 929.4; DB 4; Length 2429;  
Best Local Similarity 71.1%; Pred. No. 7.7e-253;  
Matches 1335; Conservative 0; Mismatches 491; Indels 51; Gaps 6;

QY	72	TGTTGCCTCAGTTCCTCATGATTAAGGCTCTCCGTAGAACAAATCCCAACTCTTGGA	131
Dd	89	TCGTTGATCAGTTCACGAATGTGCAGAAGGCTCTCTGTATCTTACAGCAGTCCCAACT	148
QY	132	ATCTGCAGCGCGGGAAATCCGTGCGCATTCATAAACAATGTGTTTGACAAGCGTCGCA	191
Dd	149	CTCAGAATCGTAGGCGACAGAAAAGCTCTGGTCATCAACATGAATTGACCACGTATCC	208
QY	192	TCTACTGATTCT-----GTACAGAGACGCGTGGGCAACTATCATTTCCAAC	236
Dd	209	CATCGTGATGATAATGTTGGTGGTGACTGCCAAGACGCATAGCCGATCATCATCCCAAC	268
QY	237	CTGTGGGACGATGATTCATACAGTCTCTGATCTCAACGCCTTATGGAGCACCTGATTAC	296
Dd	269	CTGTGGGAAGATGATTCATACAATCATTTGTCCTCA--CCTTATGGGGGATCTTCGTAC	325
QY	297	CGGGAACGTGCTGACAGACTTATTGGGGAAGTAAAGGATAT-----AATGTTCAAT	347
Dd	326	AGTGAACGTGCTGTGACAGTGGTTGAGGAAGTAAAGAGATGTTCAATTCATACCAAAT	385
QY	348	TTCAAGTCGCTGGAAGATGGAGGCAATGATCTCCTTCAACGACTTTTGTGTCGATGAC	407
Dd	386	AATAGAGAATATTGTTGGTCCC AAAATGATCTCCTTACACGCCTTTGGATGGTGATAGC	445
QY	408	GTTGAACGTTTGGGAATCGACAGGCAATTCAAAAAAGAGATAAAAAACGGCACTCGATTAT	467
Dd	446	ATTGAACGTTCTGGGATAGATAGACATTTCCAAAAATGAGATAAGAGTAGCCCTCGATTAT	505
QY	468	GTTAACAGTTATTGGAACGAAA---AAGGCATGGATGTGGGAGGGAGAGTGTGTGACT	524
Dd	506	GTTTACAGTTATTGGAAGGAAAAGGAAGGCATTTGGGTGTGGCAGAGATTTCTACTTTTCT	565
QY	525	GACCTCAACTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCT	584
Dd	566	GATCTCAACTCGACTGCTCTGGCGCTTCGAACTCTTCGACTGCACGGATACAATGTGTCT	625
QY	585	TCAGATGTTTGAACGTTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATT	644
Dd	626	TCAGATGTGCTGGAATACITTCAAAGATCAAAAGGGGCATTTTGGCCTGCAATCCTA	685
QY	645	CAGATAGAGGAGAGATTAGAGCGGTTCTCAATTTATTACAGGGCCTCCCTCGTCGCTTT	704



Db 1763 ATCAGAGAAATAATTGGGAGCTTCTCAGACCAGATAGCAAAAGTCCCATCTCTTCCAAG 1822  
Qy 1767 AAACAGCATTTGACATAAGCAGAGTTTGGCATCA CGGTTACAGATACCGAGATGGCTAC 1826  
Db 1823 AAACATGCTTTTGACATCACCAGAGCTTCCATCACCTCTACAAGTACCGAGATGGTTAC 1882  
Qy 1827 AGCTTTGCCAACAGTTGAACAAAGAGTTTGGTGATGAGAACCGTCAATTGAACCTGTGCCT 1886  
Db 1883 ACTGTTGCGAGTAGTGAAACAAAGAAATTGGTGATGAAACACAGTTCTTGAACCTGTGGCA 1942  
Qy 1887 TTGTAACAACACTTCAA 1903  
Db 1943 TTGTAAAAAATATCAA 1959

RESULT 13

AAx08645  
ID AAX08645 standard; cDNA; 2089 BP.

AC AAX08645;

XX 27-SEP-1999 (first entry)

XX Limonene synthase gene.

KW Mycrene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.

OS Abies grandis.

XX Key Location/Qualifiers

FT CDS 73..1986

FT /\*tag= a

FT /product= "Limonene synthase"

XX WO9902030-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014528.

XX 11-JUL-1997; 97US-0052249P.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

PI Bohlmann J, Steele CL, Croteau RB;

XX WPI; 1999-120396/10.

DR P-PSDB; AAW85702.

PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. mycrene, limonene or pinene.

PS Claim 11; Page 79-82; 121pp; English.

CC Nucleotide sequences encoding mycrene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by mycrene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal

SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Query Match

Best Local Similarity 46.0%; Score 925.4; DB 2; Length 2089;

Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;

Qy 72 TCGTGCCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTAGAAACAATCCCAACTCTTGG 131  
Db 127 TCGTTGATCAGTTCCAGCAATGTGCAGAAAGGCTCTCTGTATCTCTACAGCAGTCCCAACA 186  
Qy 132 ATCTGCAGGCCGGGAAATCCGTGCGCATTCATATAAACAATGTTTGAAGCGTCGCA 191  
Db 187 CTCAGAATCGTAGGCGACAGAAAGCTCTGGTCAATCAACATGAATGACCACCTGTATCC 246  
Qy 192 TCTACTGATTCT-----GTACAGAGACGCGTGGCAACTATCATTCACAAC 236  
Db 247 CATCGTGATGATAATGGTGGTGTACTGCAAGACCGCATAGCCGATCATCATCCCAAC 306  
Qy 237 CTGTGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTAC 296  
Db 307 CTGTGGGAAGATGATTTTCATACAAATCATTTGTCTCA---CCTATGGGGGATCTTCGTAC 363  
Qy 297 CGGAAACGTGCTGACAGACTTATTTGGGGAAGTAAAGGATAT-----AATGTTCAAT 347  
Db 364 AGTGAACGTGCTGAGACAGTCTGTGAGGAAGTAAAGAGATGTTCAATCAATACCAAT 423  
Qy 348 TTCAAGTCGCTGGAAGATGGAGCAATGATCTCTTCAACGACTTTTGTGTCGATGAC 407  
Db 424 AATAGAGAAATATTGTTTCCCAAAATGATCTCTTACACGCCCTTTGGATGGATAGC 483  
Qy 408 GTTGAACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTAT 467  
Db 484 ATTGAACGTCTGGGATAGATAGACATTTCCAAATGAGATAAGATAGCCCTCGATTAT 543  
Qy 468 GTTAACAGTTATTGGAACGAAA---AAGGCATTTGGATGTGGAGGAGAGTGTGTGACT 524  
Db 544 GTTTACAGTTATTGGAAGGAAAGGAAGGCATTTGGGTGTGGCAGAGATTTACTTTTCCT 603  
Qy 525 GACCTCAACTCAACCGCCTTGGGCTTCGAACCTCTCCGACTACACGGATACACTGTGTCT 584  
Db 604 GATCTCAACTCGACTGCCCTTGGCGCTTCGAACCTCTTCGACTGACGGATACAATGTGTCT 663  
Qy 585 TCAGATGTTTGAACGTTTTTAAAGACAAAAAATGGGCAATTTTCTCCTCCACTGCCAATATT 644  
Db 664 TCAGATGCTGCTGGAATACCTTCAAGATGAAAAGGGGCAATTTTGCTGCCCTGCAATCCTA 723  
Qy 645 CAGATAGAGGGAGAGATTAGAGGCGTTCTCAATTTATTCAGGCGCTCCCTCGTCGCTTT 704  
Db 724 ACCGAGGACAGATCACTAGAGTGTCTTAAATTTATATCGGCGCTCCCTGGTCGCTTT 783  
Qy 705 CCCGGCAGAAAAGTTATGATGAAGTGAACATCTCTACAAAAATATTAAAGAGAGGCC 764  
Db 784 CCCGGGAGAAAAGTTATGGAAGAGGCTGAAATCTTCTCGCATCTTATTGAAAAAAGTC 843  
Qy 765 CTGCAAAAAGATTCCGGCATCCAGTATACCTTTCACATAGAGATACGGGACGTTCTGGAATAT 824  
Db 844 TTACAAAAGATTCCGGTCTCCCAAT---CTTTCAGGAGAGATAGATAATGTTTGGAAATAT 900  
Qy 825 GGTTCGCACACCAATTTGCCACGCTTGAAGCAAGGAATTTACATGCGACGCTTTTGGACAG 884  
Db 901 GGTTCGCACACGAATTTGCCGAGATTGGAAGCAAGAAATTTATATCGAGGTCTACGAGCAG 960  
Qy 885 CACACTAAAAATA-----AGAACGCCGCCGAGAAACTTTTAGAACTT 926  
Db 961 AGCGGTATGAAAAGCTTAAACGAGATGCCATATATGAACATGAAGAAAGCTTTTACAACTT 1020  
Qy 927 GCAAAATTGGAATTCAATATATTTCACTCTCTTACAAAGAGAGAGATTAAACATGTTTCC 986  
Db 1021 GCAAAATTGGAGTTCAATATCTTTCACTCTTTTGCAACTTAAGAGAGTTTACAATCTATCTCC 1080  
Qy 987 CGATGTGGAAGAGACTCGGTTCTCTGATGATGACCTTCTGTGACATCGTCACGTGGAA 1046  
Db 1081 AGATGTGGAAGAAATCAGGTTCTCTCAACTGACTTTTACACGGCATCGTCACGTGGAA 1140  
Qy 1047 TACTACGCTTTGGCTTCCCTGCAATTCGTTTCGAGCCTCAACATTTGGATTTCAGACTCGGC 1106  
Db 1141 TACTACACTATGGCATCTTGCATTTCTATGTTGCCAAAACATTCAGCTTTCAGAAATGGAG 1200  
Qy 1107 TTTACCAAGATGTCTCATCTTATCAGGTTTCTTTCGACGACATGTACGACGCTCTTCGGCACA 1166

Db 1201 TTTGTCAAAGTGTGTCTATCTTGTAAACAGTTCTCGATGATATATATGACACTTTTGGAAACA 1260  
QY 1167 GTAGACGAGCTGGAACCTTTTCACAGCGACAATTAAGAGATGGGATCCGTCGCGATGGAA 1226  
Db 1261 ATGAACGAACTCCAACCTTTTACGGATGCAATTAAGAGATGGGATTTGTCAACGACAAGG 1320  
QY 1227 TGCCTTCAGAAATATATGAAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAAATG 1286  
Db 1321 TGGCTTCAGAAATATATGAAAGGAGTGTACATGATGGACTTGTATCAATGCAATTAATGAAATG 1380  
QY 1287 GCTCAGTGGCAGAGAAGGCTCAAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTGG 1346  
Db 1381 GTGGAAGAGGCTGAGAAGACTCAAGGCGGAGATATGCTCAACTATATTTCAAAATGCTTGG 1440  
QY 1347 GAGGCGTGTCTTGTATTCGTATATGCAAGGAAGCAAAAGTGGATCGCACTGGTTATCTGCC 1406  
Db 1441 GAAGCCCTATTGTATACCTTTATGCAAGAAGCAAAAGTGGATCTCCAGCAGTTATCTCCCA 1500  
QY 1407 ACGTTTGAGGAGTACTTTGGAGAACCGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTG 1466  
Db 1501 ACGTTTGAGGAGTACTTTGAAGAATGCAAAAGTTAGTTCTGTTCTGCAATAGCCACATTA 1560  
QY 1467 CAACCCATTCTGACGTTGGACATCCCTTTCCTGATCACATCCCTCAAGGAAGTTGACTTC 1526  
Db 1561 CAACCCATTCTCACTTTGGATGTACCACTTCTGTGATTACATCTGCAAGAAATTTGATTAT 1620  
QY 1527 CCATCGAAGCTCAATGACTTGTATATGTATCATCTTCCGATTAAGAGGTGATACACGGTGC 1586  
Db 1621 CCATCCAGATTCAATGAGTTAGCTTCGTCCATCCTTCGACTACGAGGTGACACGCGCTGC 1680  
QY 1587 TACAAGCAGACAGGCGCCGCTGGAGAAGAAGCTTCGTCTATATCATGTTATATGAAAGAC 1646  
Db 1681 TACAAGCGGATAGGCGCCGCTGGAGAAGAAGCTTCAGCTATATCGTGTATATGAAAGAC 1740  
QY 1647 AATCCTGGATTAAACGGAAGAGATGCTCTGAATCATATCATCACTTCATGATCAGGACGCA 1706  
Db 1741 CATCCTGATCAATAGAGGAAGATGCTCTCAATCATATCAACGCCATGATCAGTGATGCA 1800  
QY 1707 ATCAGAGAATTAATTTGGGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCACTTCCAG 1766  
Db 1801 ATCAGAGAATTAATTTGGGAGCTTCTCAGACCGGATAGCAAAAGTCCCATCTCTTCCAG 1860  
QY 1767 AAACACGCAATTTGACATAAGCAGAGTTTGGCATCAAGGTTACAGATACCGAGATGGCTAC 1826  
Db 1861 AAACATGCTTTTGACATCACAGAGCTTTCCATCATGTCTACAAATATCGAGATGGTTAC 1920  
QY 1827 AGCTTTGCCAACGTTGAAACAAAGAGTTTGGTGTATGAGAACCGTCAATTGAACCTGTGCT 1886  
Db 1921 ACTGTTTCCAAACAAACGAAACAAAGAAATTTGGTGTATGAAACCGTTCTTGAACCTCTCGCT 1980  
QY 1887 TTGTAACAACACTTCAAAATCTACAATATTAATTAAGG 1923  
Db 1981 TTGTAAAAACATATAGATGCAATGCAATTAATAATGTGGGAAG 2017

RESULT 14  
AAA38938  
ID AAA38938 standard; DNA; 2089 BP.  
XX  
AC AAA38938;  
XX  
DT 25-AUG-2000 (first entry)  
XX  
DE Grand fir limonene synthase DNA sequence SEQ ID NO:57.  
XX  
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;  
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;  
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;  
KW defensive agent; pigment; antitumour; steroid hormone;  
KW signal transduction pathway; bile acid; affinity purification;  
KW photoreceptor; enzymatic synthesis; nutrient supplement;  
KW immunological reagent; ds.

XX  
OS Abies grandis.  
XX  
PN WO200017327-A2.  
XX  
PD 30-MAR-2000.  
XX  
PF 17-SEP-1999; 99WO-US021419.  
XX  
PR 18-SEP-1998; 98US-0100993P.  
PR 22-APR-1999; 99US-0130628P.  
PR 23-AUG-1999; 99US-0150262P.  
XX  
PA (KENT ) UNIV KENTUCKY RES DEPT.  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Chappell J, Manna KR, Noel JP, Starks CM;  
XX  
DR WPI; 2000-292839/25.  
DR P-PSDB; AAY90859.  
XX  
PT Novel terpene synthase enzymes, useful for producing terpene  
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known  
PT enzymes by specific amino acid alterations.  
XX  
PS Disclosure; Page 445-448; 450pp; English.  
XX  
CC The present invention describes an isolated terpene synthase (I)  
CC comprising a region with at least 20% identity to region 265-535 of a 548  
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha  
CC -carbon atoms (alphaC) that have interatomic distances, between each  
CC other, within tabulated ranges, have a centre point (within a sphere of  
CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered  
CC arrangement of R groups (defining aa side chains), excluding specific  
CC tabulated arrangements (tables given in the specification). (I), and  
CC related enzymes, are used to produce a wide range of terpenoids (e.g.  
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,  
CC flavours, pheromones, defensive agents, pigments, antitumour agents,  
CC components of signal transduction pathways, precursors of steroid  
CC hormones and bile acids, as photoreceptors and as co-factor side chains.  
CC Some synthases with little or no catalytic activity (and nucleic acids  
CC encoding them) are used as controls in the analysis of products formed by  
CC enzymatic synthesis; as nutrient supplements; for affinity purification  
CC of isoprenoids; or to develop immunological reagents or nucleic acids for  
CC monitoring expression of terpene synthase or inheritance of the gene in  
CC plant breeding programs. The new synthases may produce novel terpene  
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Query Match 46.0%; Score 925.4; DB 3; Length 2089;  
Best Local Similarity 70.6%; Pred. No. 9.8e-252;  
Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;

QY 72 TCGTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCTTGA 131  
Db 127 TCGTTGATCAGTTCCAGCAATGTGCAGAGGCTCTCTGTATCTTACAGCAGTCCCAACA 186  
QY 132 ATCTGCAGGCCGGGAAATCCGTCGCGCATTCCTATAAACATGTGTTTGACAAGCGTCGCA 191  
Db 187 CTCAGAAATCGTAGGCGACAGAAAGCTCTGGTCATCAACATGAATTGACCCTGTATCC 246  
QY 192 TCTACTGATTCT-----GTACAGAGACGGGTGGGCAACTATCATTCACAAC 236  
Db 247 CATCGTGATGATAATGGTGGTGTACTGCAAGACGATAGCCGATCATCATCCCAAC 306  
QY 237 CTGTGGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTAC 296  
Db 307 CTGTGGGAAGATGATTTTCATACATCATTTGTCCTCA---CCTTATGGGGATCTTCGTAC 363  
QY 297 CGGAAACGTGCTGACAGACTTATTTGGGGAAGTAAGGATAT-----AATGTTCAAT 347

Db 364 AGTGAACGTGCTGAGACAGTCGTTGAGGAAGTAAAGAGATGTTCAATTCAATACCAAAAT 423

QY 348 TTCAAGTCGCTGGAAGATGAGAGGCAATGATCTCCTTCAACGACTTTTGTGTTGTCGATGAC 407

Db 424 AATAGAGAAATTAATTTGGTTCCCAAAATGATCTCCTTACACGCCCTTTGGATGGTGATAGC 483

QY 408 GTTGAACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTAT 467

Db 484 ATTGAACGTCCTGGGATAGATAGACATTTCCAAAATGAGATAAGAGTAGCCCTCGATTAT 543

QY 468 GTTAAACAGTTATTGGAACGAAA--AAGGCATTGGATCTGGGAGGGAGAGTGTTCGTGACT 524

Db 544 GTTTACAGTTATTGGAAGGAAAAGGAAGGCAATTGGGTGTGGCAGAGATTCTACTTTTCCT 603

QY 525 GACCTCAACTCAACCGCCTTTGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCT 584

Db 604 GATCTCAACTCGACTGCCCTTGGCGCTTCGAACTCTTCGACTGCACGGATACAATGTGCT 663

QY 585 TCAGATGTTTTGAACGTTTTTAAAGACAAAAAATGGGCAATTTTCCTCCACTGCCAATATT 644

Db 664 TCAGATGTGCTGGAATACTTCAAAGATGAAAAGGGCAATTTTGCTGCCCTGCAATCCTA 723

QY 645 CAGATAGAGGGAGAGATTAGAGCGCTTCTCAATTTATTAGGGCCCTCCCTCGTCGCCTTT 704

Db 724 ACCGAGGGACAGATCACTAGAAGTGTCTTAATTTTATATCGGGCTTCCCTGGTCGCCTTT 783

QY 705 CCCGGCGAGAAAGTTATGGATGAAGCTGAAACATTTCTTACAAAAATATTTAAGAGAAAGCC 764

Db 784 CCCGGGAGAAAGTTATGGAAGAGGCTGAAATCTTCTCGGCATCTTATTTGAAAAAAGTC 843

QY 765 CTGCAAAAGATTCCGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTCGGAATAT 824

Db 844 TTACAAAAGATTCCGCTCTCCAAT---CTTTCAGGAGAGATAGAATATGTTTTGGAATAT 900

QY 825 GGTGGCACACCAATTTGACAGCTTGGAGCAAGGAATTACATGGACGCTTTTGGACAG 884

Db 901 GGTGGCACACGAATTTGCCGAGATTGGAAGCAAGAAATATATCGAGGCTTACGAGCAG 960

QY 885 CACACTAAAAATA-----AGAACGCCGCCGAGAAAACITTTTAGAACTT 926

Db 961 AGCGGCTATGAAAGCTTAAACGAGATGCCATATATGAACATGAAGAAGCTTTTACAACTT 1020

QY 927 GCAAAAATTGGAATTCATATATTTTCACTCCTTTACAAGAGAGAGAGTTAAAAACATGTTTCC 986

Db 1021 GCAAAAATTGGAGTTCAATATCTTTTCACTCTTTTGCAACTAAGAGAGTTACAATCTATCTCC 1080

QY 987 CGATGGTGAAAAGACTCGGTTCTCCTGAGATGACCTTCTGTGCAGATCGTCACGTGGAA 1046

Db 1081 AGATGGTGAAAAGAAATCAGGTTCTGTCTCAACTGACTTTTACACGGCATCGTCACGTGGAA 1140

QY 1047 TACTACGCTTTGGCTTCCTCGCATTCGTTTCGAGCCTCAACATTTCTGGATTCAGACTCGGC 1106

Db 1141 TACTACACTATGGCATCTGTCATTTCTATGTTGCCAAAACATTCAGCTTTCAGAATGGAG 1200

QY 1107 TTTACCAAGATGTCTCATCTTATCAGCGTTCTTGACGACATGTACGACGTCITTCGGCACA 1166

Db 1201 TTTGTCAAAGTGTGTCTCTTGTAAACAGTTCTCGATGATATATATGACACTTTTGGAAACA 1260

QY 1167 GTAGACGAGCTGGAACCTTTCACAGCGACAAATTAAGAGATGGGATCCGTCCGCGATGGAA 1226

Db 1261 ATGAACGAACTCCAACTTTTACGGATGCAATTAAGAGATGGGATTTGTCAACGACAAGG 1320

QY 1227 TGCCTTCAGAAATATATGAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAAATG 1286

Db 1321 TGGCTTCAGAAATATATGAAGGAGTGTACATGGACTTGTATCAATGCAATTAATGAAATG 1380

QY 1287 GCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGG 1346

Db 1381 GTGGAAGAGGCTGAGAAGACTCAAGGCCGAGATATGCTCAACTATATTTCAAAATGCTTGG 1440

QY 1347 GAGGCGTGTTTTGATTCGTATATGCAGGAAGCAAAAGTGGATCGCCACTGGTTATCTGCC 1406

Db 1441 GAAGCCCTATTTTGATACCTTTATGCAAGAAGCAAAAGTGGATCTCCAGCAGTTATCTCCA 1500

QY 1407 ACGTTTGAGGAGTACTTTGGAGAACGGGAAAAGTTAGTCTTGTCTATCGCCCATCGGCACTG 1466

Db 1501 ACGTTTGAGGAGTACTTTGAAGAATGCAAAAAGTTAGTCTTGGTTCTCGCATAGCCACATTA 1560

QY 1467 CAACCCATTCTGACGTTGGACATCCCCTTTTCCCTGATCACATCCTCAAGGAAAGTTGACTTC 1526

Db 1561 CAACCCATTCTCACTTTGGATGTACCACTTCCCTGATTACATACTGCAAGAAATTGATTAT 1620

QY 1527 CCATCGAAGCTCAATGACTTGATATGTATCATCCTTCGATTAAAGAGGTGATACACGGTGC 1586

Db 1621 CCATCCAGATTCAATGAGTTAGCTTCGTCCATCCTTCGACTACGAGGTGACACGCGCTGC 1680

QY 1587 TACAAGGCAGACAGGCCCGTGGAGAAGAGCTTCGTCTATATCATGTTTATATGAAAGAC 1646

Db 1681 TACAAGGCGGATAGGCCCGTGGAGAAGAGCTTCAGCTATATCGTGTATATGAAAGAC 1740

QY 1647 AATCCTGGATTAAACGGAAGAAGATGCTCTGAATCATATCAACTTCATGATCAGGACGCA 1706

Db 1741 CATCCTGGATCAATAGAGGAAGATGCTCTCAATCATATCAACGCCATGATCAGTGATGCA 1800

QY 1707 ATCAGAGAAATTAATTTGGGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCATTCCAAG 1766

Db 1801 ATCAGAGAAATTAATTTGGGAGCTTCTCAGACCCGGATAGCAAAAGTCCCATCTCTTCCAAG 1860

QY 1767 AAACACGCATTTGACATAAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTAC 1826

Db 1861 AAACATGCTTTTGACATCACAGAGCTTTCATCATGTCTACAAATATCGAGATGGTTAC 1920

QY 1827 AGCTTTGCCAACGTTTGAACAAAAGAGTTTGGTGTGATGAGAACCGTCAATTGAACCTGTGCCT 1886

Db 1921 ACTGTTTCCAAACAACGAAACAAAAGAATTTGGTGTATGAAAAACCGTTCTTTGAACCTCTCGCT 1980

QY 1887 TTGTAACAAACACTTCAAAATCTACAATATTAACTGAGG 1923

Db 1981 TTGTAACAAACATATAGAATGCATTAAATGTGGGAAG 2017

RESULT 15

AAF73373

ID AAF73373 standard; cDNA; 2089 BP.

XX AAF73373;

AC AAF73373;

XX 30-APR-2001 (first entry)

DT Grand fir (-)-limonene synthase coding sequence SEQ ID NO: 5.

XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;

DE myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;

XX terpinolene synthase; insect resistance; nutrition; ss.

OS Abies grandis.

XX WO200107565-A2.

PN 01-FEB-2001.

XX 24-JUL-2000; 2000WO-US020264.

XX 26-JUL-1999; 99US-00360545.

PF (UNIW ) UNIV WASHINGTON STATE RES FOUND.

PA Steele CL, Bohlmann J, Croteu RB, Phillips MA;

XX WPI; 2001-182782/18.

DR P-PSDB; AAB69372.

XX New nucleic acid encoding monoterpene synthases, for increasing terpene

PT synthesis in plants, e.g. for increasing resistance to pests or for

PT treatment of cancer.

XX



PS Claim 33; Page 112-115; 175pp; English.

XX The present invention provides the protein and coding sequences of

CC monoterpene synthases from the grand fir. These include (-)-camphene

CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-

CC limonene, (-)-alpha-pinene synthase, limonene synthase, myrcene synthase

CC and pinene synthase. The sequences can be used to produce transgenic

CC plants expressing high levels of the enzymes, resulting in levels which

CC are useful in protecting against and treating cancers, and to confer

XX insect resistance on plants

SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Query Match 46.0%; Score 925.4; DB 4; Length 2089;

Best Local Similarity 70.6%; Pred. No. 9.8e-252;

Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;

QY 72 TCGTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTTTGGA 131

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

127 TCGTTGATCAGTCCAGCAATGTGCAGAAAGGCTCTCTGTATCTCTACAGCAGTCCCAACA 186

QY 132 ATCTGCAGGCCGGGAAATCCGTGCGGCATTCCATAAACAATGTGTTTGACAAGCGTCGCA 191

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

187 CTCAGAAATGCGTAGGCCAGACAAAGCTCTGGTTCATCAACATGAATTGACCACGTATCC 246

QY 192 TCTACTGATTCT-----GTACAGAGACCGGTGGGCAACTATCATCTCCAAC 236

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

247 CATCGTGATGATAATGGTGGTGTACTGCAAGACGCATAGCCGATCATCATCCCAAC 306

QY 237 CTGTGGGACGATGATTTCAATACAGTCTCTGATCTCAACGCCTTATGGAGCACCTGATTAC 296

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

307 CTGTGGGAAGATGATTTTCAATACATCATTTGTCTCA---CCTTATGGGGATCTCGTAC 363

QY 297 CGGGAACGTCTGACAGACTTATTGGGGAAGTAAAGGATAT-----AATGTTCAAT 347

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

364 AGTGAACGTGCTGAGACAGTCTGTGAGGAAGTAAAGAGATGTTCAATTCAATACCAAAAT 423

QY 348 TTCAAGTCGCTGGAAGATGGAGCAATGATCTCCTTCAACGACTTTTGTGTCGATGAC 407

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

424 AATAGAGAATTATTGTTGTTCCCAAATGATCTCCTTACACGCCTTTGGATGGTGGATAGC 483

QY 408 GTTGAACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCAGCTCGATTAT 467

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

484 ATTGAACGTCCTGGGATAGATAGACATTTCCAAATGAGATAAGAGTAGCCCTCGATTAT 543

QY 468 GTTAACAGTTATTGGAACGAAA--AAGGCATTGGATGTGGGAGGGAGAGTGTGTGACT 524

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

544 GTTTACAGTTATTGGAAGAAAAGGAAGGCAATTGGGTTGGCAGAGATTCTACTTTTCCT 603

QY 525 GACCTCAACTCAACCGCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCT 584

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

604 GATCTCAACTCGACTGCCCTGGCGCTTCGAACTCTTCGACTGCACGGATACAATGTGTCT 663

QY 585 TCAGATGTTTGAACGTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATT 644

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

664 TCAGATGTCTGGAATACTTCAAAGATGAAAAGGGGCAATTTGCTGCTGCCCTGCAATCCTA 723

QY 645 CAGATAGAGGGAGAGATTAGAGGCGTTCTCAATTTATTAGGGGCTCCCTCGTCGCTTT 704

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

724 ACCGAGGACAGATCACTAGAAGTGTCTAAATTTTATCGGGCTTCCCTGGTCGCTTT 783

QY 705 CCCGGCGAGAAAGTTATGGAAGCTGAAACATTTCTTACAAAATATTTTAAGAGAAGCC 764

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

784 CCCGGGAGAAAGTTATGGAAGAGGCTGAAATCTTCTCGGCATCTTATTTGAAAAAGTC 843

QY 765 CTGCAAAAGATTCCGGCATCCAGTATATCTTCACTAGAGATACGGGACGTTCTGGAATAT 824

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

844 TTACAAAAGATTCCGGTCTCCAAT---CTTTACAGAGAGATAGAATATGTTTGGAAATAT 900

QY 825 GGTGGCACACCAATTTGCCACGCTTGGGAAGCAAGGAATTACATGGACGCTCTTTGGACAG 884

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

901 GGTGGCACACGAATTTGCCGAGATTGGAAGCAAGAAATATATATCGAGGTCTACGAGCAG 960

QY 885 CACACTAAAAATA-----AGAACGCCGCCGAGAAAACTTTTAGAACTT 926

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

961 AGCGGCTATGAAAAGCTTAAACGAGATGCCATATATGAACATGAAGAAGCTTTTACAACTT 1020

QY 927 GCAAAATTGGAATTCATATATTTTCACTCTTTACAAGAGAGAGATTAAAAACATGTTTCC 986

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1021 GCAAAATTGGAGTTCAATATCTTTCACTCTTTGCAACTAAGAGAGTTACAATCATCTCTCC 1080

QY 987 CGATGGTGGAAAGACTCGGGTTCTCCTGAGATGACCTTCTGTGACATCGTCACGTGGAA 1046

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1081 AGATGGTGGAAAGATCAGGTTCTCTCAACTGACTTTTACACGGCATCGTCACGTGGAA 1140

QY 1047 TACTACGCTTTGGCTTCTGTCATTGCGTTTCGAGCCCTCAACATTTCTGGATTCTGACTCGGC 1106

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1141 TACTACACTATGGCATCTTGCAATTTCTATGTTGCCAAAAACATTCAGCTTTTCAAGATGGAG 1200

QY 1107 TTTACCAAGATGTCTCATCTTATCACGGTTCTTGACGACATGTACGACGTTCTTCGGCACA 1166

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1201 TTTGTCAAAGTGTGTCTTGTAAACAGTTCTCGATGATATATGACACTTTTGGAAACA 1260

QY 1167 GTAGACGAGCTGGAACCTTTTACAGCGACAATTAAGAGATGGATCCGTCCGCGATGGAA 1226

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1261 ATGAACGAACTCCAACTTTTACGGATGCAATTAAGAGATGGGATTTGTCAACGACAAGG 1320

QY 1227 TGCCTTCCAGAAATATATGAAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAAATG 1286

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1321 TGGCTTCCAGAAATATATGAAAGGAGTGTACATGGACTTGTATCAATGCATTAATGAAATG 1380

QY 1287 GCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGG 1346

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1381 GTGGAAGAGGCTGAGAAAGACTCAAGGCCGAGATATGCTCAACTATATTCAAATGCTTGG 1440

QY 1347 GAGGCGTGTGTTGATTCGTATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCC 1406

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1441 GAAGCCCTATTGATACCTTATGCAAGAAAGCAAGTGGATCTCCAGCAGTTATCTCCA 1500

QY 1407 ACGTTTGAGGAGTACTTTGGAGAACGGGAAAGTTAGTCTCTGCTCATCGCCCATCGGCACTG 1466

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1501 ACGTTTGAGGAGTACTTTGAAGAAATGCAAAAGTTAGTTCTGCTCGCATAGCCCATTA 1560

QY 1467 CAACCCATTCTGACGTTGGACATCCCCTTTTCTGTATCATCTTCGATCACTCTCAAGGAAGTTGACTTC 1526

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1561 CAACCCATTCTCATTGATGTACCACCTTCCCTGATTACATACTGCAAGAAATGATTAT 1620

QY 1527 CCATCGAAGCTCAATGACTTGATATGATCATCTTCGATTAAGAGGTGATACACGGTGC 1586

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1621 CCATCCAGATTCAATGAGTTAGCTTCGTCCATCTTCGACTACGAGGTGACACGCGCTGC 1680

QY 1587 TACAAGGCAGACAGGCCGCTGGAGAAGAGCTTCGCTCTATATCATGTTTATATGAAGAC 1646

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1681 TACAAGCGGATAGGCCGCTGGAGAAGAGCTTCAGCTATATCGTGTATATGAAGAC 1740

QY 1647 AATCCTGGATTAAACGGAAGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCA 1706

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1741 CATCCTGGATCAATAGGAAGATGCTCTCAATCATATCAACGCCATGATCAGTGATGCA 1800

QY 1707 ATCAGAGAAATTAATTGGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCTTCCAAG 1766

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1801 ATCAGAGAAATTAATTGGAGCTTCTCAGACCCGATAGCAAAAGTCCCATCTCTTCCAAG 1860

QY 1767 AAACACGCATTTGACATAAGCAGAGTTTGGCATCA CGGTTACAGATACCGAGATGGCTAC 1826

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1861 AAACATGCTTTTGACATCACAGAGCTTTCCATCATGTCTACAAATATCGAGATGTTTAC 1920

QY 1827 AGCTTTGCCAACGTTGAAAAAAGAGTTTGGTGTAGAGAACCGTCAATTGAACCTGTGCTT 1886

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1921 ACTGTTTCCAAACAACGAAACAAAGAAATTTGGTGTAGAAACCGTCTTCTGAACCTCTCGCT 1980

QY 1887 TTGTAACAACACACTTCAATCTACAATATTAACAGG 1923

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1981 TTGTAACAAACATATAGATGTCATTAAAATGTGGGAAG 2017



Search completed: July 8, 2004, 12:35:48  
Job time : 918.973 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 8, 2004, 11:16:49 ; Search time 6169.26 Seconds  
(without alignments)  
9743.880 Million cell updates/sec

Title: US-10-025-145A-64  
Perfect score: 2013  
Sequence: 1 ttttgacgtgccttttcttc.....aaaaaaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_mam: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrl: \*  
28: gb\_gss1: \*  
29: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564.2	28.0	745	14 CF477103	CF477103 RTWW3_5_A
2	475.2	23.6	697	13 BQ196773	BQ196773 NXLV105_B
3	447.2	22.2	599	13 BX680641	BX680641 BX680641
4	428.2	21.3	599	12 BG526917	BG526917 NXPV_057_

5	427	21.2	700	14	CF474786	CF474786 RTWW2_7_B
6	425.8	21.2	637	14	CF476978	CF476978 RTWW3_5_A
7	419.2	20.8	696	14	CF401916	CF401916 RTWW1_15_
8	413	20.5	669	14	CF479802	CF479802 RTWW3_12_
9	399.6	19.9	616	14	CF663845	CF663845 RTCNT1_5_
10	388.6	19.3	516	13	BQ698077	BQ698077 NXPV_064_
11	384.4	19.1	517	13	BX677624	BX677624 RTWW3_12_
12	384.2	19.1	804	14	CF666338	CF666338 RTCNT1_22
13	376	18.7	481	9	AL750951	AL750951 AL750951
14	375	18.6	740	14	CF477562	CF477562 RTWW3_8_G
15	352.4	17.5	539	10	AW287756	AW287756 EST0004_S
16	343.8	17.1	557	14	CF666483	CF666483 RTCNT1_23
17	339.8	16.9	651	14	CF479884	CF479884 RTWW3_12_
18	327.4	16.3	682	14	CF663768	CF663768 RTCNT1_5_
19	324.8	16.1	534	10	AW287755	AW287755 EST0003_S
20	315.4	15.7	569	10	AW287754	AW287754 EST0002_S
21	312.2	15.5	430	13	BQ702557	BQ702557 NXSI_129
22	302.4	15.0	591	14	CA305371	CA305371 hasp004xx
23	300.4	14.9	541	14	CF672979	CF672979 RTCNT1_75
24	284.2	14.1	618	9	AL750955	AL750955 AL750955
25	283.6	14.1	542	10	BG039521	BG039521 NXSI_099
26	264	13.1	574	14	CF474640	CF474640 RTWW2_7_B
27	264	13.1	733	14	CF666270	CF666270 RTCNT1_22
28	245.4	12.2	574	9	AW065088	AW065088 ST39E04_P
29	239	11.9	597	14	CF666416	CF666416 RTCNT1_23
30	215.4	10.7	385	10	AW697531	AW697531 ST64A12_P
31	211.6	10.5	725	14	CF470471	CF470471 RTDS1_17_
32	197.4	9.8	634	14	CF397946	CF397946 RTDS3_23_
33	197.2	9.8	725	14	CF397293	CF397293 RTDS3_2_A
34	193.2	9.6	353	14	CA305444	CA305444 hasp015xd
35	188.6	9.4	552	13	BQ696735	BQ696735 NXPV_044_
36	187.8	9.3	529	13	BQ698322	BQ698322 NXPV_068_
37	185	9.2	400	14	CF672970	CF672970 RTCNT1_75
38	181.8	9.0	601	9	AW043070	AW043070 ST28H10_P
39	181.2	9.0	530	9	AU298829	AU298829 AU298829
40	180.6	9.0	597	9	AW011129	AW011129 ST17A09_P
41	176.6	8.8	629	9	AU299287	AU299287 AU299287
42	176.2	8.8	487	14	Z92688	Z92688 SCI571/1_No
43	164	8.1	306	10	AW226490	AW226490 ST82H11_P
44	162.4	8.1	730	13	BX682869	BX682869 BX682869
45	156.6	7.8	580	9	AU298828	AU298828 AU298828

ALIGNMENTS

RESULT 1  
CF477103  
LOCUS  
DEFINITION  
CF477103 745 bp mRNA linear EST 08-SEP-2003  
RTWW3\_5\_A06.g1\_A022 Well-watered loblolly pine roots WW3 Pinus  
taeda\_cDNA clone RTWW3\_5\_A06\_A022 5', mRNA sequence.  
ACCESSION  
CF477103  
VERSION  
CF477103.1 GI:34505972  
KEYWORDS  
EST.  
SOURCE  
Pinus taeda (loblolly pine)  
ORGANISM  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus;  
REFERENCE  
1 (bases 1 to 745)  
AUTHORS  
Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J.,  
Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and  
Neale,D.  
TITLE  
An EST database from well-watered loblolly pine (Pinus taeda) roots  
JOURNAL  
Unpublished (2003)  
COMMENT  
Other\_ESTs: RTWW3\_5\_A06.b1\_A022  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
RNA prepared and library constructed by W. Walter Lorenz, School of

Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: JENREV (CAGGAACACGCTATGACC).

FEATURES		Location/Qualifiers	
source		1..745	
		/organism="pinus taeda"	
		/mol_type="mRNA"	
		/strain="CCLONES"	
		/db_xref="taxon:3352"	
		/clone="RTW3 5 A06_A022"	
		/lab_host="DH10B-T1 phage-resistant E. coli"	
		/clone_lib="Well-watered loblolly pine roots WW3"	
		/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."	
ORIGIN			
Query Match		28.0%; Score 564.2; DB 14; Length 745;	
Best Local Similarity		84.8%; Pred. No. 6e-90;	
Matches	632;	Conservative	0; Mismatches 113; Indels 0; Gaps 0;
QY	1100	ACTCGGCTTTACCAAGATGTCATCTTATCACGGTCTTGACGACATGTACGACGTCTT	1159
Db	1	ACTCGGCTTTGCCAAATCCTGTCTATATCATCACCGTCTTGTATGATATGTACGACACCTT	60
QY	1160	CGGCACAGTAGACGAGCTGGAACCTCTTCACAGCGACAATTAAGAGATGGGATCCGTCGCG	1219
Db	61	CGGAACACTCGACGAGCTCGAACTCTTCACAGCTGCAATTAAGAGATGGGATCCGTCGCG	120
QY	1220	GATGGAATGCCTTCCGAATATATGAAAGGAGTGATGATGTTTATCACACCGTAA	1279
Db	121	GACAGAGTGCCCTTCCAGAATATATGAAAGGAGTTTACATGATGTTTACAACACTGTAA	180
QY	1280	TGAAATGGCTCGAGTGGCAGAGAAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACA	1339
Db	181	TGAAATGTCTCAGGAGCGACACAAGGCTCAAGGCCGAGACACGCTCAACTATTGTGACA	240
QY	1340	GGCTTGGGAGCGGTGTTTGATTCGTATATGCAGGAAGCAAAAGTGGATCGCCACTGGTTA	1399
Db	241	GGCTTGGGAGGAATATATGATTCGTATATGCAAGAACAAAGTGGATCGCCAGTGGTGA	300
QY	1400	TCTGCCACGTTTGAGGAGTACTTGGAGAACGGGAAGTGTAGCTCTGTCTATCGCCCATG	1459
Db	301	GGTGCCAAACATTTGAGGAGTACTACGAGAACGGGAAAATAGCTCTGTCTATCGCGTATC	360
QY	1460	CGCACTGCAACCCATTCTGACGTTGGACATCCCTTTCTCTGATCACATCCTCAAGGAAGT	1519
Db	361	GGCAATTGCAACCCATTCTGACGACCGACATCCCTTTCTCTGAGCACGTCCTCAAGGAAGC	420
QY	1520	TGACTTCCCATCGAAGCTCAATGACTTGATATGTATCATCTTTCGATTAGAGGTGATAC	1579
Db	421	TGACATTCCATCGAAGCTCAATGACTTGGCATCTGCCATCTTCGATTACGAGGAGATAC	480
QY	1580	ACGGTGCTACAAGGCAGACAGGCCCGCTGGAGAAGAGCTTCGTCTATATCATGTTATAT	1639
Db	481	CGCTGCTACACGGCGGACAGGCCCGCTGGAGAAGAGCTTCGTGTATATCTTTGTTATAT	540
QY	1640	GAAAGACAATCCTGGATTAAACGGAAGAAGATGCTCTGATCATATCAACTTCATGATCAG	1699
Db	541	GAAAGACAATCCTGGAGCAACGGAAGAAGATGCTCTCATCATATCAACGCCATGATCAG	600
QY	1700	GGACGCAATCAGAGAAATTAATTGGGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATAC	1759
Db	601	TGATGTAATTAAGGATTAAATTGGGAGCTTCTCAAAACCAACAGCAGCGTTCCCATATC	660

QY	1760	TTCCAAGAAACACGCAATTGACATAGACAGAGTTTGGCATCACGGTTACAGATACCGAGA	1819
Db	661	TGCCAAAAACATGCTTTTGACATTAGCAGAGCTTCCATTATGGCTACAAATATCGAGA	720
QY	1820	TGGCTACAGCTTTGCCAACGTTGAA	1844
Db	721	TGGCTACAGCGTTGCCAGCATTGAA	745
RESULT 2			
BQ196773			
LOCUS			
DEFINITION			
BQ196773			
NXLV105_B02_F NXLV (Nsf Xylem Late wood Vertical) Pinus taeda linear EST 07-MAY-2003			
clone NXLV105_B02_5' similar to Arabidopsis thaliana sequence			
At4g16730 limonene cyclase like protein see			
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.			
BQ196773			
BQ196773.1 GI:20379276			
EST.			
Pinus taeda (loblolly pine)			
ORGANISM			
Pinus taeda			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.			
REFERENCE			
1 (bases 1 to 697)			
Sederoff,R.			
AUTHORS			
Molecular Basis of Wood Formation in the Pine Megagenome			
Unpublished (2000)			
JOURNAL			
COMMENT			
Contact: Sederoff, Ron			
Forest Biotechnology			
North Carolina State University			
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,			
NC 27695, USA			
Tel: 919 515 7800			
Fax: 919 515 7801			
Email: ron.sederoff@ncsu.edu, jerri.johnson@ncsu.edu			
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further			
information.			
Seq primer: T3.			
FEATURES		Location/Qualifiers	
source		1..697	
		/organism="Pinus taeda"	
		/mol_type="mRNA"	
		/strain="Coastal plain loblolly pine from North Carolina"	
		/db_xref="taxon:3352"	
		/clone="NXLV105_B02"	
		/tissue_type="primary xylem"	
		/dev_stage="late wood"	
		/lab_host="XL1-Blue"	
		/clone_lib="NXLV (Nsf Xylem Late wood Vertical)"	
		/note="Vector: pTriplex; Site 1: EcoRI; The library is from late (summer-August) wood, taken from below the crown of a 20 year old tree. The harvested xylem tissue was on the the cusp between transitional and mature wood. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCCATTATGGCC'."	
ORIGIN			
Query Match		23.6%; Score 475.2; DB 13; Length 697;	
Best Local Similarity		83.0%; Pred. No. 3.3e-74;	
Matches	534;	Conservative	0; Mismatches 109; Indels 0; Gaps 0;
QY	1250	AGTGTCATGATGGTTTATCACACCGTAAATGGAATGGCTCGAGTGGCAGAGAAGCTCA	1309
Db	22	AGTTTACATGATAGTTTACAACACTGTAATGAATGTCTCAGGAGGCAGACAGGCTCA	81
QY	1310	AGCCCGAGACACGCTCAACTATGCAAGACAGCGCTTGGAGCGGTGTTTGTATCGTATAT	1369
Db	82	AGCCCGAGACACGCTCAACTATTGTTCACAGGCTTGGAGGAATATATTGATGCGTATAT	141
QY	1370	GCAGGAAGCAAAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAGGAGTACTTGGAGAA	1429
Db	142	GCAAGAAGCAAAAGTGGATCGCCCGTGGTGAGTGAGTGCCCAACATTTGAGGAGTACTATGAGAA	201





Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron.sederoff@ncsu.edu, jerri.johnson@ncsu.edu  
Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further information.

Seq primer: T3.

```
Location/Qualifiers
1. .599
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXPV 057 D04"
/tissue_type="Xylem"
/cell_type="Planings (secondary)"
/dev_stage="Transitional"
/lab_host="XL1-Blue"
/clone_lib="NXPV (Nsf Xylem Planings wood Vertical)"
/notes="Vector: Bluescript SK; Site_1: Eco RI; Site_2:
XhoI; The library is from early (spring) secondary wood,
taken from a ten year old tree in the transitional phase.
The tree is a kind gift of the Westvaco Corporation.
Secondary xylem was harvested from the tree by peeling
back the bark and primary xylem and then removing the
underlying tissue with a block plane. NOTE: The sequences
contain a 'cDNA adapter' between the EcoRI site and the
start of the EST. The adapter sequence is
'AAATCGGACCGAG' "
```

ORIGIN

Query Match 21.3%; Score 428.2; DB 12; Length 599;  
Best Local Similarity 80.9%; Pred. No. 7e-66;  
Matches 484: Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY	1216	CGCGATGGAATGCCCTTCCAGAAATATATGAAGGAGTGTACATGATGTTTATCACACCG	1277
Db	1	CGCGACACAGTGCCTTCCAGAAATATGAAGGAGTGTACATGATAGTTTACAACTG	60
QY	1276	TAAATGAAATGGCTCGAGTGGCAGAGAAAGGCTCAAGGCCGAGACACGCTCAACTATGCAA	1335
Db	61	TAAATGAAATGTCTCAGGAGGCAGACAAGGCTCAAGGCCGAGACACGCTCAACTATTGTC	120
QY	1336	GACAGGCTTGGGAGGCGTGTTTTGATTTCGTATATCCAGGAAGCAAAGTGGATCGCCACTG	1395
Db	121	GACAGGCTTGGAGGAAATATATTGATGCGTATATGCAAGAAAGCAAAGTGGATCGCCAGTG	180
QY	1396	GTTATCTGCCACAGTTTGAGGAGTACTTGGAGAACGGGAAAAGTTAGTCTGTCTCATCGCC	1455
Db	181	GTGAGGTGCCAACATTTGAGGAGTACTATGAGAACGGGAAAAGTTAGTCTGTGTCATCGCG	240
QY	1456	CATCGGCACGTCAACACCCATTTCTGACGTTGGACATCCCTCTTCTGATCACATCCTCAAGG	1515
Db	241	TATCGGCATTGCAACCCATTTTGACGACCGACATCCCTTTCTTGAGCACGTCCTCAAGG	300
QY	1516	AAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGTATCATCTTCGATTAAGAGGTG	1575
Db	301	AAGTTGACTTCCATCGCAGCTCAATGACTTGGCATCTGCCATTCTTCGATTACGAGGGG	360
QY	1576	ATACACGGTGTACAAGGCAGACAGGGCCCGTGGAGAAGAAGCTTCGTCTATATCATGTT	1635
Db	361	ATACGCGCTGTACCNNGCGACAGGGCCCGTGGAGAAGAAGCTTCGTGTATATCTTGTT	420
QY	1636	ATATGAAAGACAATCCTGGATTAAACGGAAGAAGATGCTCTGAAATCATATCAACTTCATGA	1695
Db	421	ATATGAAAGACAATCCTNNAAACAACAGAGGAAGATGCTCTCAATCATCTCAACGCCATGA	480
QY	1696	TCAGGGACGCAATCAGAGAAATTAAATTGGGAGCTTCTAAAAGCCAGACAACAGTGTCCCA	1755
Db	481	TCAGTGATGTTATTANANNNTTAAATTGGGAGCTTCTCAAAACCAACAGCAGCGTCCCA	540
QY	1756	TCACCTTCCAAGAAAACACGCAATTTGACATAAGCAGAGTTTGGCATCACGGTTACAGATA	1813
Db	541	TATCTGCCAAAANNNCATGCTTTTGACATTANCNNNNNNNNTCCNNNTGTGGCTACAAATA	598

RESULT 5	CF474786	CF474786	linear	EST 05-SEP-2003
LOCUS	RTWW2_7_B11.g1_A021	Well-watered loblolly pine roots WW2	Pinus	
DEFINITION	taeda_cDNA clone RTWW2_7_B11_A021	5', mRNA sequence.		
ACCESSION	CF474786			
VERSION	GI:34492158			
KEYWORDS	EST.			
SOURCE	Pinus taeda (loblolly pine)			
ORGANISM	Pinus taeda			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 700)			
AUTHORS	Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebrenedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.			
TITLE	An EST database from well-watered loblolly pine (Pinus taeda) roots			
JOURNAL	Unpublished (2003)			
COMMENT	Other ESTs: RTWW2_7_B11.b1_A021			
	Contact: Cordonnier-Pratt MM			
	Laboratory for Genomics and Bioinformatics			
	The University of Georgia, Department of Plant Biology			
	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA			
	Tel: 706 542 1860			
	Fax: 706 583 0210			
	Email: mmpratt@uga.edu			
	RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.			
	Seq primer: JENREV (CAGGAACAGCTATGACC).			

FEATURES  
SOU

## ORIGIN

	Query Match	21.2%;	Score 427;	DB 14;	Length 700;
	Best Local Similarity	75.7%;	Pred. No. 1.1e-65;		
	Matches 529;	Conservative	0;	Mismatches 170;	Indels 0; Gaps 0;
QY	1034	TCGTACGTTGGAATACTACGCTTTTGGCTTCCTGCAATTGCGTTCGAGCCTCAACATTCTGG	1093		
DB	1	TCGTACGTTGGAATACTACACTTTAGCAGCTTGCAATTGCAAAATGATCCTAAACATTCTGC	60		
QY	1094	ATTCAGACTCGGCTTTTACCAAGATGTCTCATCTTATCACGGTTCTTGACGACATGTACGA	1153		
DB	61	GTTTCGACTAGGATTTGGTAAATAAGTCATATGATCACGATTCTCGACGATATCTACGA	120		
QY	1154	CGTCTTCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACAATTAAGAGATGGGATCC	1213		
DB	121	CACCTTCGGAAACAATGGAGGAGCTCGAACTCTTAACCGCAGCGTTTAAGAGATGGGATCC	180		
QY	1214	GTCCGCGATGGAATGCCTTCCAGAATATATGAAAGGAGTGTCATGATGGTTTATCACAC	1273		
DB	181	GTCTTCGATAGAGTGTCTTCCAGATTATATGAARAGGAGTGTACATGGCGGGTTTACGACAA	240		





Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.  
An EST database from well-watered loblolly pine (Pinus taeda) roots  
Unpublished (2003)  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: JENREV (CAGGAACACGCTATGACC).

FEATURES  
source

Location/Qualifiers  
1..696  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTW1\_15\_B05\_A015"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WW1"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 20.8%; Score 419.2; DB 14; Length 696;  
Best Local Similarity 75.1%; Pred. No. 2.6e-64;  
Matches 523; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 1065 TGCATTGCGTTCGAGCCTCAACATTCTGGATTTCAGACTCGGCTTTACCAAGATGTCTCAT 1124  
Db 1 TGCATTGCAAAATGATCTCAACATTTTGCGTTTCGACTAGGATTTGGTAAATAAGTCAT 60  
QY 1125 CTTATCACGGTCTTGACGACATGTACGAGCTTCGCGCACAGTAGACGAGCTGGAATC 1184  
Db 61 ATGATCACGATTCTCGACCATATCTACGACACCTTCGGAACAATGGAGGAGCTCGAACTC 120  
QY 1185 TTCACAGCGACAATTAAGAGATGGGATCCGTCGCGGATGAATGCCTTCCAGAAATATG 1244  
Db 121 TTAACCGCAGCGTTTAAGAGATGGGATCCGTTCTCGATAGAGTGTCTTCCAGATTATG 180  
QY 1245 AAAGGAGTGATCATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAAG 1304  
Db 181 AAAGGAGTGATCATGGCGTTTACGACAACATCAACGAAATGGCACGAGAGGCGCAGAAA 240  
QY 1305 GCTCAAGCGCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTTTTGATTCG 1364  
Db 241 ATTCAAGCTGGGATACACTCAGCTATGCTCGAAAATCTTGGAGGCTTTTATIGTGCT 300  
QY 1365 TATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCCCACGTTTGAGGAGTACTTG 1424  
Db 301 TATATACAAGAGCAAGTGGATTCCAGTGGTTATCTTCCACGTTTCGACGAGTACCTC 360  
QY 1425 GACAACGGGAAAGTTAGTCTGCTCATCGCCCCATCGCACTGCAACCCATTCTGACGTTG 1484  
Db 361 GAGAAATGGGAAGGTCAGCTTCGGCTCTCGCATAAACACGCTCGAACCCATGCTGACTTG 420  
QY 1485 GACATCCCTTTTCTGTATCATATCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGAC 1544  
Db 421 GGGTTTCTCTTCCGCTCGAATCTCGAGGAAATGACTTTCATCGAAATTCATGAT 480

QY 1545 TTGATATGTATCATCCTTCGATTAAAGAGGTGATACACGGTGCTACAAGGACAGAGGGCC 1604  
Db 481 TTGATATGTGCATCCTTCGACTGAAAGGTGACACTCAATGCTACAAGGTGACAGGGCG 540  
QY 1605 CGTGGAGAAAGAGCTTCGTCTATATCATGTTATATGAAAGACAATCCTGGATTAAACGAA 1664  
Db 541 CGTGGAGAAAGAGCTTCGGCCGTATCGTGTATATGAAAGACCATCTCGAATAACAGAG 600  
QY 1665 GAAGATGCTCTGAATCATATCAACTTCATGATCAGGACGCAATCAGAGAATTAATTTG 1724  
Db 601 GAAGATGCTGTCAATCAAGTCAATGCTATGTCGATAACTTAACCAAGGAATGAATTGG 660  
QY 1725 GAGCTTCTAAGCCAGACAACAGTGTTCCTCCATCACT 1760  
Db 661 GAGTTACTTAGACCCGACAGCGGTGTTCCTCCATCTCT 696

RESULT 8

CF479802/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF479802 669 bp mRNA linear EST 08-SEP-2003  
RTWW3\_12\_D02.b1\_A022 Well-watered loblolly pine roots WW3 Pinus  
taeda\_cDNA clone RTWW3\_12\_D02\_A022 3', mRNA sequence.

CF479802

CF479802.1 GI:34508671

EST.

Pinus taeda (loblolly pine)

Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

1 (bases 1 to 669)

Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J.,

Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J.,

Cannon,R., Owen,A. and Neale,D.

EST database from well-watered loblolly pine (Pinus taeda) roots

Unpublished (2003)

Other ESTs: RTWW3\_12\_D02.g1\_A022

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

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Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of

Forestry, University of Georgia; plant material prepared at the

University of Florida; sequencing done in the Laboratory for

Genomics and Bioinformatics, University of Georgia. Sequence ends

have been trimmed to exclude vector and regions below Phred quality

16. Three-prime sequences are presented as their reverse complement

and have been trimmed to exclude polyA.

Seq primer: M13-21 (TGTAACACGACGCGCCAGT)

POLYA=No.

Location/Qualifiers

1..669

/organism="Pinus taeda"

/mol\_type="mRNA"

/strain="CCLONES"

/db\_xref="taxon:3352"

/clone="RTWW3\_12\_D02\_A022"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Well-watered loblolly pine roots WW3"

/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The

library was prepared from polyA+ RNA from loblolly pine

(Pinus taeda) roots watered to pot capacity every other

day. Pre-dawn water potential remained -0.3 MPa +/-0.1.

Roots were harvested for RNA isolation. Double-stranded

cDNA was cloned unidirectionally into pSL1180. Inserts

excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 20.5%; Score 413; DB 14; Length 669;  
Best Local Similarity 76.1%; Pred. No. 3.3e-63;  
Matches 509; Conservative 0; Mismatches 160; Indels 0; Gaps 0;





Db 491 GGAAGAAGCAAGTGGATGTCACGCGGTATATATACCCACGTTTGAGGAGTATTGGAGAA 550  
QY 1430 CGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTTGGACAT 1489  
Db 551 CGGGAAGTGAGTTTGGGTATCGAGCAGCCACACTGCAACCCATTCTCAGTTGGATAT 610

QY 1490 CCCCTT 1495  
Db 611 TCCCCT 616

RESULT 10  
BQ698077  
LOCUS BQ698077 516 bp mRNA linear EST 07-MAY-2003  
DEFINITION NXPV\_064\_C05\_F NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda  
CDNA clone NXPV\_064\_C05\_5, similar to Arabidopsis thaliana sequence  
At1961680 hypothetical protein see  
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.

ACCESSION BQ698077  
VERSION BQ698077.1 GI:21823393  
KEYWORDS EST.  
SOURCE Pinus taeda (loblolly pine)

ORGANISM Pinus taeda  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
AUTHORS Sederoff,R.  
TITLE Molecular Basis of Wood Formation in the Pine Megagenome  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron.sederoff@ncsu.edu, jerri.johnson@ncsu.edu  
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further  
information.

Seq primer: T3.  
FEATURES Location/Qualifiers  
source 1. .516  
/organism="pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXPV\_064\_C05"  
/tissue\_type="Xylem"  
/cell\_type="Planings (secondary)"  
/dev\_stage="Transitional"  
/lab\_host="X11-Blue"  
/clone\_lib="NXPV (Nsf Xylem Planings wood Vertical)"  
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:  
XhoI; The library is from early (spring) secondary wood,  
taken from a ten year old tree in the transitional phase.  
The tree is a kind gift of the Westvaco Corporation.  
Secondary xylem was harvested from the tree by peeling  
back the bark and primary xylem and then removing the  
underlying tissue with a block plane. NOTE: The sequences  
contain a 'cDNA adapter' between the EcoRI site and the  
start of the EST. The adapter sequence is  
'AATTCGGCACGAG'."

ORIGIN

Query Match 19.3%; Score 388.6; DB 13; Length 516;  
Best Local Similarity 84.7%; Pred. NO. 7.3e-59;  
Matches 436; Conservative 0; Mismatches 79; Indels 0; Gaps 0;  
QY 1353 TGTGTTGATTGATGAGGAAGCAAAAGTGGATCGCCACTGGTTATCTGCCACGTTT 1412  
Db 2 TATATTGATCGGTATATGCAAGAAGCAAAAGTGGATCGCCAGTGGTGCCACATT 61

QY 1413 GAGGAGTACTTGGAGAACGGGAAAGTTAGCTCTGCTCATGCCCCATGCGCACTGCAACCC 1472  
Db 62 GAGGAGTACTATGAGAACGGGAAAGTTAGCTCTGCTCATGCGGTATCGGCATTGCAACCC 121  
QY 1473 ATTCTGACGTTGGACATCCCCTTTTCTGATCACATCCTCAAGGAAGTTGACTTCCCATCG 1532  
Db 122 ATTTTGACGACCGACATCCCCTTTTCTGAGCACGCTCCTCAAGGAAGTTGACATTCATCG 181  
QY 1533 AAGCTCAATGACTTGATATGATATCATCTTCGATTAAAGAGGTGATACACGGTGCTACAAG 1592  
Db 182 CAGCTCAATGACTTGGCATCTGCCATTCTTCGATTACGAGGGGATACGCGTGCTACCAG 241  
QY 1593 GCAGACAGGCGCGTGGAGAAGAGCTTCGCTATATCATGTTATATGAAAAGACAATCCT 1652  
Db 242 CGGACAGGCGCGTGGAGAAGAGCTTCGCTATATCTTGTATATGAAAAGACAATCCT 301  
QY 1653 GGATTAAACGGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGA 1712  
Db 302 GGAACAACAGAGGAAGATGCTCTCAATCATCTCAACGCCCATGATCAGTGATGTAATTA 361  
QY 1713 GAATTAAATTGGAGCTTCTAAAGCCAGACAACAGATGTTCCCATCATCTCAAGAAACAC 1772  
Db 362 GGATTAAATTGGAGCTTCTCAAAACCAACAGCAGCGTTCCCATATCTGCCAAAAACAT 421  
QY 1773 GCATTGACATAAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTT 1832  
Db 422 GCTTTTGACATTAGCAGAGCTTTCATTGTGGCTACAAATATCGAGATGGCTACAGCGTT 481  
QY 1833 GCCAACGTTGAAACAAAGAGTTTGGTGATGAGAAC 1867  
Db 482 GCCAACATTGAAACAAAGAGTTTGGTGAGAGAAC 516

RESULT 11  
BX677624

LOCUS BX677624  
DEFINITION BX677624 RN Pinus pinaster cDNA clone RN42B08, mRNA sequence.  
ACCESSION BX677624  
VERSION BX677624.1 GI:38011576  
KEYWORDS EST.  
SOURCE Pinus pinaster

ORGANISM Pinus pinaster  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
AUTHORS Frigerio,J. and Plomion,C.  
TITLE Identification of water-deficit responsive genes in Maritime pine  
(Pinus pinaster Ait.) using an EST approach  
JOURNAL Unpublished (2002)  
COMMENT Contact: Frigerio JM  
Genetique et Amelioration 69  
INRA

route d'Arcachon 33612 Cestas CEDEX France  
Email: Frigerio@pierroton.inra.fr  
Email: Frigerio@pierroton.inra.fr  
Seq primer: T3.

FEATURES Location/Qualifiers  
source 1. .517

/organism="Pinus pinaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:71647"  
/clone="RN42B08"  
/tissue\_type="root"  
/dev\_stage="6 weeks old seedling"  
/lab\_host="SOLR"  
/clone\_lib="RN"  
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library  
was made from the roots of 6 weeks old seedlings grown in  
hydroponic conditions. A mixture of genotypes were used.  
Oligo-dT primed cDNA was directionally cloned into the  
EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form  
a pBluescript phagemid"

ORIGIN

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Query Match      19.1%; Score 384.4; DB 13; Length 517;
Best Local Similarity 85.1%; Pred. No. 4e-58;
Matches 441; Conservative 0; Mismatches 76; Indels 1; Gaps 1;

QY 1215 TCCGCGATGAATGCCTTCCAGAAATATATGAAAGGAGTGATCATGATGGTTTATCACACC 1274
Db 1 TCGCGCAGAGTGCCTTCCAGAAATATATGAAAGGAGT-TACATGATAGTTTACAACT 59

QY 1275 GTAAATGAAATGGCTCGAGTGGCAGAGAAAGGCTCAAGCGCGAGACACGCTCAACTATGCA 1334
Db 60 ATAAATGAAATGTCTCAGGAGGCAGACAAAGGCTCAAGCGCGAGACACGCTCAACTATTGT 119

QY 1335 AGACAGGCTTGGGAGGCGTGTGTTTTCGTTATTCGTATATGAGGAAGCAAAGTGGATCGCCACT 1394
Db 120 CGACAGGCTTGGGAGGAATATATGATGCGTATATGCAAGAAGCAAAGTGGATCGCCAGT 179

QY 1395 GGTATCTGCCCCAGTTTGAGGAGTACTTTGGAGAACGGGAAAAGTTAGCTCTGCTCATCGC 1454
Db 180 GGTGAGGTGCCAACATTTGAGGAGTACTATGAGAACGGGAAAAGTTAGCTCTGCTCATCGC 239

QY 1455 CCATGCGCACTGCAACCCATTTGACGTTGGACATCCCTTTCTCTGATCACATCCTCAAG 1514
Db 240 GTATCGGCATTGCAACCCATTCTGACGACCGACATCCCTTTCTTGAGCACGCTCCTCAAG 299

QY 1515 GAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGATATCATCTTCGATTAAGAGGT 1574
Db 300 GAAGTGGACATTCCTCGAAGCTCAATGACTTGGCATCTGCCATTCTTCGATTACGAGGG 359

QY 1575 GATACACGGTGTCTACAGGCAGACAGGCGCCGTCGAGAGAAGCTTCGTCATATCATGT 1634
Db 360 GACACTCGCTGTACCAGCGGACAGAGGCCCCGTGGAGAAGAAGCTTCGCGTATATCTTGT 419

QY 1635 TATATGAAAGACAATCTCGGATTAACGGAAGAGATGCTCTGAATCATATCAACTTCATG 1694
Db 420 TATATGAAAGACAATCTCGGAAACAACAGAGGAAGATGCTCTCAATCATATCAACGCCATG 479

QY 1695 ATCAGGGACGCAATCAGAGAAATTAATTTGGGAGCTTCT 1732
Db 480 ATCAGTGAATGAATTAAGAGATTAAATTTGGGAGCTTCT 517
```

```
RESULT 12
CF666338
LOCUS
DEFINITION
  RTCNT1_22_C05.g1_A029 Root control Pinus taeda cDNA clone
  RTCNT1_22_C05_A029 5', mRNA sequence.
ACCESSION
  CF666338
KEYWORDS
  Pinus taeda (loblolly pine)
SOURCE
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
    Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Zimmermann,C. and
    Dean,J.F.D.
    An EST database from untreated loblolly pine (Pinus taeda) roots
    Unpublished (2003)
    Other_ESTs: RTCNT1_22_C05.b1_A029
    Contact: Cordonnier-Pratt MM
    Laboratory for Genomics and Bioinformatics
    The University of Georgia, Department of Plant Biology
    Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
    Tel: 706 542 1860
    Fax: 706 583 0210
    Email: mmpratt@uga.edu
    RNA prepared and library constructed by W. Walter Lorenz (School of
    Forest Resources, University of Georgia); plant material prepared
    by Craig Zimmermann (School of Forest Resources, University of
    Georgia) using rooted cuttings provided by the Forest Biology
    Research Cooperative (FBRC) and the CCLONES project at the
    University of Florida; sequencing done in the Laboratory for
```

Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAAACAGCTATGACC).

Location/Qualifiers

1..804

/organism="Pinus taeda"

/mol\_type="mRNA"

/strain="3 CCLONES"

/db\_xref="taxon:3352"

/clone="RTCNT1\_22\_C05\_A029"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Root control"

/note="Organ: root; Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Just before harvesting roots for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 19.1%; Score 384.2; DB 14; Length 804;  
Best Local Similarity 75.0%; Pred. No. 3.7e-58;  
Matches 556; Conservative 0; Mismatches 158; Indels 27; Gaps 5;

QY 68 CAGGTCGTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT 127  
Db 67 CAGAACGTTGTTTCGGTTTGTAGTCATGAGCTGAAAGCTATCCATAGTACAGTCCCAAATCT 126

QY 128 TGAATCTGCAGGCGGGGAAATCCGTCGCGCATTCCTATAAACATGTGTGTGACAAAGCGT 187  
Db 127 TGGAAATGTGCAGGGGAGGGAATCCATAGCACCTTCTATGAGCATGAGTTGACCCACTC 186

QY 188 CGCATCTACT---GATTCTGTACAGAGACGCGTGGGCAACTATCATTTCCACCTGTGGGA 244  
Db 187 CGTTTCTAATGAGGATGGGTACCAAGACGCGATAGCTGGTCATCATTTCCAACTTTGGGA 246

QY 245 CGATGATTTTCATACAGTCTCTGATCTCAACGCTTATGGAGCACCTGATACCGGGAACG 304  
Db 247 CGATGATTTCCATAGCCTCTC---TCTCCACTTCTATGAGGCACCTTCTTACCGTAAGCG 303

QY 305 TGCTGACAGACTTATTGGGGAAGTAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGA 364  
Db 304 CGCTGATAAACTTATAGGGGAAGTAAGAAAT---ATCTTCGATTTAATGTCAGTGGAGGA 360

QY 365 TGGAG-----GCAATGATCTCCTTCAACGACTTTTGTGCTGGTTCGATGACGT 409  
Db 361 TGGAGTATTACACAGTCCCTCAGTGACCTCCATCACCCTCTGGATGGTTCGATAGCGT 420

QY 410 TGAACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGT 469  
Db 421 TGAACGTTTGGGAATCGATAGGCATTTCAAAAGACGAGATAAAATTCCTCTGGATCATGT 480

QY 470 TAACAGTTATTGGAACGAAAAAGGCATTTGGATGTGGGAGGAGAGTGTGTGACTGACCT 529  
Db 481 TTACAGTTATTGGACCGAAAAAGGCATTTGGACGTGGCAGAGAAAGTGGTGTGACTGATCT 540

QY 530 CAACTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGA 589  
Db 541 CAACTCAACTGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACAGTGTCTTCACA 600

QY 590 TGTTTTCAGACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATTCAGAT 649  
Db 601 TGTTCTGATCACTTCAAAAAACGAGAAAGGGCAGTTTACTTGTCTCTGCC---ATTCAAAC 657

QY 650 AGAGGGAGAGATTAGAGGCGTTTCTCAATTTATTTCAGGGCGCTCCCTCGTCGCCTTCCCCG 709



Db	658	AGAGGAGAGATAAGAGATGTCCTCAATTATTTCGGGCATCTCTCATTCGCTTTCTCTGG	717
QY	710	CGAGAAAGTTATGGATGAAGCTGAACATCTCTACAAATATTTAAGAGAAAGCCCTGCA	769
Db	718	CGAAAAAATTATGGAGCGGCTGAAATCTTCTCTACAATGTATTTAAAGATGCCCTACA	777
QY	770	AAAGATTCGGGCATCCAGTAT	790
Db	778	AAAGATTCGGCCCTCCGGTCT	798
RESULT 13			
LOCUS	AL750951		
DEFINITION	AL750951 RS Pinus pinaster cDNA clone RS02D01 similar to PINENE		
ACCESSION	AL750951		
KEYWORDS	SYNTHASE, mRNA sequence.		
SOURCE	AL750951.1 GI:21492198		
ORGANISM	EST.		
REFERENCE	Pinus pinaster		
AUTHORS	Pinus pinaster		
TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus. 1 (bases 1 to 481)		
JOURNAL	Frigerio, J. and Plomion, C.		
COMMENT	Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach		
UNPUBLISHED (2002)			
CONTACT: FRIGERIO JM			
GENETIQUE ET AMELIORATION 69			
INRA			
ROUTE D'ARCACHON 33612 CESTAS CEDEX FRANCE			
EMAIL: FRIGERIO@PIERROTON.INRA.FR			
SEQ PRIMER: T3.			
LOCATION/QUALIFIERS			
1. .481			
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/clone="RS02D01"			
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/dev_stage="6 weeks old seedling"			
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/clone_lib="RS"			
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"			
ORIGIN			
Query Match	18.7%;	Score 376;	DB 9; Length 481;
Best Local Similarity	86.5%;	Pred. No. 1.3e-56;	
Matches	415;	Conservative 0;	Mismatches 65; Indels 0; Gaps 0;
QY	1038	CACGTGGAATACTACGCTTTGGCTTCCTGCATTGCGTTCGAGCCTCAACATTCGTGATTC	1097
Db	2	CACGTGGAGTACTACACTTTGGCTTCCTGCATCGCGTTTGAGCCCCAACATTCGTGATTC	61
QY	1098	AGACTCGGCTTTACCAAGATGTCTCATCTTATCACGGTTCCTTGACGACATGTACGACGTC	1157
Db	62	AGACTCGGCTTTGCGAAAGCGTGTATATTATCATCTGTCTTCGACGATATGTACGACCTC	121
QY	1158	TTCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACAATTAAGAGATGGATCCGTC	1217
Db	122	TTCGGAACAGTTGATGAGCTCAAAGTGTTCACAGCGCAATTAAGAGATGGATCCGTC	181
QY	1218	CGGATGGAATGCCCTTCAGAATATATGAAAGGAGTGATCATGATGTTTATCACACCGTA	1277

Db	182	GCCACAGATTGCCTTCCACAATATATGAAAGGAATTTACATGATGGTTTACAACACCGTA	241
QY	1278	AATGAAATGGCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGA	1337
Db	242	AATGAAATGTCTCGGAGGCCACAGAAAGGCTCAAGGCCGAGACACTCTCAACTATGCTCGA	301
QY	1338	CAGGCTTGGGAGGCGTGTTTTGATTTCGTATATGCAGGAAGCAAAGTGATGCCACTGGT	1397
Db	302	CAGGCTTGGGAGGATTATCTTGATTTCGTATATGCAAGAAGCAAAGTGATGCCACGGGT	361
QY	1398	TATCTGCCACGTTTGAGGAGTACTTTGGAGAACGGGAAAGTTAGTCTCTCATCGCCCA	1457
Db	362	TATCTGCCAACGTTTCGAGGAATACTTTGGAGAACGGGAAAGTTAGTCTTGGGCATCGCGTG	421
QY	1458	TGCGCACTGCACCCATTCTGACGTTTGACATCCCTTTCTCTGATCATCTCAAGGAA	1517
Db	422	TCGGCGTTGCAACCCCATGCTGACGATGGACATCCCCCTTTCTCTCATCTCAAGGAA	481
RESULT 14			
CF477562/c	CF477562 740 bp mRNA linear EST 08-SEP-2003		
LOCUS	RTWW3_8 G10_g1_A022 Well-watered loblolly pine roots WW3 Pinus		
DEFINITION	taeda cDNA clone RTWW3_8_G10_A022 5', mRNA sequence.		
ACCESSION	CF477562		
VERSION	CF477562.1 GI:34506431		
KEYWORDS	EST.		
SOURCE	Pinus taeda (loblolly pine)		
ORGANISM	Pinus taeda		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus. 1 (bases 1 to 740)		
AUTHORS	Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.		
TITLE	An EST database from well-watered loblolly pine (Pinus taeda) roots		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Cordonnier-Pratt MM		
Laboratory for Genomics and Bioinformatics			
The University of Georgia, Department of Plant Biology			
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA			
Tel: 706 542 1860			
Fax: 706 583 0210			
Email: mmpratt@uga.edu			
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.			
Seq primer: JENREV (CAGGAAACAGCTATGACC).			
FEATURES			
Location/Qualifiers			
1. .740			
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/mol_type="mRNA"			
/strain="CCCLONES"			
/db_xref="taxon:3352"			
/clone="RTWW3_8 G10_A022"			
/lab_host="DH10B-T1 phage-resistant E. coli"			
/clone_lib="Well-watered loblolly pine roots WW3"			
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."			
ORIGIN			
Query Match	18.6%;	Score 375;	DB 14; Length 740;
Best Local Similarity	76.1%;	Pred. No. 1.6e-56;	





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 8, 2004, 12:09:59 ; Search time 1054.29 Seconds  
(without alignments)  
9305.868 Million cell updates/sec

Title: US-10-025-145A-64  
Perfect score: 2013  
Sequence: 1 ttttgacgtgcctttcttc.....aaaaaaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2013	100.0	2013	15	US-10-025-145A-64
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3	1306.8	64.9	2018	9	US-09-903-012-19
4	1306.8	64.9	2018	10	US-09-900-797-19
5	1306.8	64.9	2018	13	US-09-893-820-19
6	1306.8	64.9	2018	14	US-10-041-007-21
7	1306.8	64.9	2018	15	US-10-025-145A-3
8	1092.4	54.3	1890	15	US-10-025-145A-77
9	1072.4	53.3	2186	15	US-10-025-145A-66
10	1071.6	53.2	2196	9	US-09-887-586A-29
11	1071.6	53.2	2196	9	US-09-903-012-29
12	1071.6	53.2	2196	10	US-09-900-797-29
13	1071.6	53.2	2196	13	US-09-893-820-29
14	1071.6	53.2	2196	14	US-10-041-007-25

15	1071.6	53.2	2196	15	US-10-025-145A-1	Sequence 1, Appli
16	1071.6	53.2	2205	15	US-10-025-145A-31	Sequence 31, Appl
17	929.4	46.2	2429	14	US-10-041-007-27	Sequence 27, Appl
18	929.4	46.2	2429	15	US-10-025-145A-68	Sequence 68, Appl
19	925.4	46.0	2089	9	US-09-887-586A-57	Sequence 57, Appl
20	925.4	46.0	2089	9	US-09-903-012-57	Sequence 57, Appl
21	925.4	46.0	2089	10	US-09-900-797-57	Sequence 57, Appl
22	925.4	46.0	2089	13	US-09-893-820-57	Sequence 57, Appl
23	925.4	46.0	2089	14	US-10-041-007-23	Sequence 23, Appl
24	925.4	46.0	2089	15	US-10-025-145A-5	Sequence 5, Appli
25	471	23.4	696	15	US-10-025-145A-70	Sequence 70, Appl
26	445.8	22.1	1865	9	US-09-887-586A-47	Sequence 47, Appl
27	445.8	22.1	1865	9	US-09-903-012-47	Sequence 47, Appl
28	445.8	22.1	1865	10	US-09-900-797-47	Sequence 47, Appl
29	445.8	22.1	1865	13	US-09-893-820-47	Sequence 47, Appl
30	445.8	22.1	1865	14	US-10-041-007-17	Sequence 17, Appl
31	429.6	21.3	1967	15	US-10-025-145A-17	Sequence 17, Appl
32	427	21.2	2700	9	US-09-887-586A-43	Sequence 43, Appl
33	427	21.2	2700	9	US-09-903-012-43	Sequence 43, Appl
34	427	21.2	2700	10	US-09-900-797-43	Sequence 43, Appl
35	427	21.2	2700	12	US-10-041-018-363	Sequence 363, App
36	427	21.2	2700	13	US-09-893-820-43	Sequence 43, Appl
37	391.6	19.5	2424	9	US-09-887-586A-45	Sequence 45, Appl
38	391.6	19.5	2424	9	US-09-903-012-45	Sequence 45, Appl
39	391.6	19.5	2424	10	US-09-900-797-45	Sequence 45, Appl
40	391.6	19.5	2424	13	US-09-893-820-45	Sequence 45, Appl
41	391.6	19.5	2424	14	US-10-041-007-14	Sequence 14, Appl
42	391.6	19.5	2424	15	US-10-025-145A-15	Sequence 15, Appl
43	391.6	19.5	2528	14	US-10-041-007-13	Sequence 13, Appl
44	390.2	19.4	1785	9	US-09-887-586A-49	Sequence 49, Appl
45	390.2	19.4	1785	9	US-09-903-012-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-10-025-145A-64

; Sequence 64, Application US/10025145A

; Publication No. US20030175861A1

; GENERAL INFORMATION:

; APPLICANT: Croteau, Rodney B.

; APPLICANT: Bohlmann, Joerg

; APPLICANT: Steele, Christopher L.

; APPLICANT: Phillips, Michael A.

; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)

; FILE REFERENCE: WSUR18414

; CURRENT APPLICATION NUMBER: US/10/025,145A

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: US 09/360,545

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: PCT/US98/14528

; PRIOR FILING DATE: 1998-07-10

; PRIOR APPLICATION NUMBER: US 60/052,249

; PRIOR FILING DATE: 1997-07-11

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64

; LENGTH: 2013

; TYPE: DNA

; ORGANISM: Abies Grandis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (36)..(1889)

; OTHER INFORMATION:

US-10-025-145A-64

Query Match 100.0%; Score 2013; DB 15; Length 2013;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGACGTGCCTTCTTATCTGATAGCAAGCTGAATGGCTCTTCTTTCTATTACTCCGC 60  
|||||

Db 1 TTTTGACGTGCTTCTTATCTGATAGCAAGCTGAAATGGCTCTTCTTTCTATTACTCCGC 60

QY 61 TGGTTTCCAGGTCGTGCCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCC 120

Db 61 TGGTTTCCAGGTCGTGCCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCC 120

QY 121 CAACTCTTGGAAATCTGCAGGCCGGGGAATCCGTCGCGCATTCOCATAAACAATGTGTTGA 180

Db 121 CAACTCTTGGAAATCTGCAGGCCGGGGAATCCGTCGCGCATTCOCATAAACAATGTGTTGA 180

QY 181 CAAGCGTCGCATCTACTGATTCTGTACAGAGACCGCTGGGCAACTATCAATCCAACTGT 240

Db 181 CAAGCGTCGCATCTACTGATTCTGTACAGAGACCGCTGGGCAACTATCAATCCAACTGT 240

QY 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCCGG 300

Db 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCCGG 300

QY 301 AACGTGCTGACAGACTTATTTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGG 360

Db 301 AACGTGCTGACAGACTTATTTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGG 360

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Db 361 AAGATGGAGGCAATGATCTCCTTCAACGACTTTTGGTGGTGCATGACGTTGAACGTTTGG 420

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Db 421 GAATCGACAGGCATTTCAAAAAGAGATATAAAAACGGCACTCGATTATGTTAAACAGTTATT 480

QY 481 GGAACGAAAAAGGCAATGGATGTGGGAGGGAGACTGTTGTGACTGACCTCAACTCAACCG 540

Db 481 GGAACGAAAAAGGCAATGGATGTGGGAGGGAGACTGTTGTGACTGACCTCAACTCAACCG 540

QY 541 CCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGTTTGAACG 600

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Db 601 TTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCGCAATATTTCAGATAGAGGGAGAGA 660

QY 661 TTAGAGGCGTTCTCAATTTATTCAGGGCCTCCCTCGCTGCTTCCCGCGAGAAAGTTA 720

Db 661 TTAGAGGCGTTCTCAATTTATTCAGGGCCTCCCTCGCTGCTTCCCGCGAGAAAGTTA 720

QY 721 TGGATGAAGCTGAACATTTCTACAAAATATTTAAGAGAAGCCCTGCAAAAGATTCGG 780

Db 721 TGGATGAAGCTGAACATTTCTACAAAATATTTAAGAGAAGCCCTGCAAAAGATTCGG 780

QY 781 CATCCAGTATACCTTTCATAGAGATACGGGACGTTCTGGAATATGTTGGCACACCAATT 840

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Db 841 TGCCACGCTTGGAGCAAGGAATTACATGGACGTCCTTGGACAGCACACTAAATAAGA 900

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Db 901 ACGCCGCCGAGAACTTTTAGAACTTGCAAAATTTGGAATTCATATATTTCACTCCTTAC 960

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Db 961 AAGAGAGAGAGTTAAAAACATGTTTCCCGATGGTGGAAAGACTCGGGTTCTCCTGAGATGA 1020

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Db 1021 CCTTCTGTCGACATCGTCAAGGAACTACTACGCTTTGGCTTCCCTGCAATGCGTTCGAGC 1080

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Db 1081 CTCACATTTCTGGATTCAGACTCGGCTTTTACCAAGATGCTCATCTTATCACGGTCTTG 1140

QY 1141 ACGACATGTACGACGTCTTCCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACAATTA 1200

Db 1141 ACGACATGTACGACGTCTTCCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACAATTA 1200

QY 1201 AGAGATGGGATCCGTCGCGGATGGAAATGCGCTTCCAGAAATATATGAAGGAGTGTACATGA 1260

Db 1201 AGAGATGGGATCCGTCGCGGATGGAAATGCGCTTCCAGAAATATATGAAGGAGTGTACATGA 1260

QY 1261 TGGTTTATCACACCGTAAATGAAATGGCTTCGAGTGGCAGAGAAAGCTCAAGGCCGAGACA 1320

Db 1261 TGGTTTATCACACCGTAAATGAAATGGCTTCGAGTGGCAGAGAAAGCTCAAGGCCGAGACA 1320

QY 1321 CGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTTTTGATTCGTATATGAGGAAAGCAA 1380

Db 1321 CGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTTTTGATTCGTATATGAGGAAAGCAA 1380

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Db 1381 AGTGGATCGCCACTGGTTATCTGCCCCACGTTTGGAGAGTACTTGGAGAACGGGAAAGTTA 1440

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Db 1621 CGTCTATATCATGTTATGAAAGACAAATCCTGGATTAAACGGAAGAGATGCTCTGAATC 1680

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Db 1681 ATATCAACTTCATGATCAGGGACGCAATCAGAGAAATTAATTTGGAGCTTCTAAAGCCAG 1740

QY 1741 ACAACAGTGTTCCTCATCACTTCCAAGAAACACGCAATTTGACATAAGCAGAGTTTGGCATC 1800

Db 1741 ACAACAGTGTTCCTCATCACTTCCAAGAAACACGCAATTTGACATAAGCAGAGTTTGGCATC 1800

QY 1801 ACGGTTACAGATACCGAGATGGCTACAGCTTTCGCAACGTTGAAAACAAAGAGTTTGGTGA 1860

Db 1801 ACGGTTACAGATACCGAGATGGCTACAGCTTTCGCAACGTTGAAAACAAAGAGTTTGGTGA 1860

QY 1861 TGAGAACCGTCAATGAAACCTGTGCCTTTGTAAACAACACTTCAAATCTACAATATTAACCTG 1920

Db 1861 TGAGAACCGTCAATGAAACCTGTGCCTTTGTAAACAACACTTCAAATCTACAATATTAACCTG 1920

QY 1921 AGGATGCCCTATGGTGTATATAGGGCACACAAAAATAAATATGTTTGTGTAGTAAAGC 1980

Db 1921 AGGATGCCCTATGGTGTATATAGGGCACACAAAAATAAATATGTTTGTGTAGTAAAGC 1980

QY 1981 TGTAATTTATGAAAAAAGGAAAAAAGGAAAAA 2013

Db 1981 TGTAATTTATGAAAAAAGGAAAAAAGGAAAAA 2013

RESULT 2  
US-09-887-586A-19  
; Sequence 19, Application US/09887586A  
; Patent No. US20020094556A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094556A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001



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; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
;
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-887-586A-19

Query Match      64.9%; Score 1306.8; DB 9; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY 68 CAGGTCGTGCCTCAGTCTCTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT 127
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Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 188 CGCATCTACTGATCTGTACAGAGACGCGTGGCAACTATCATTCCAACCTGTGGGACGA 247
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 248 TGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGGAACGTGC 307
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 308 TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG 367
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 368 AG-----GCAATGATCTCCTTCAACGACTTTTGTGTCGATGACGTTGA 412
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 413 ACGTTTGGGAATCGACAGGCATTTCAAAAAGAGATAAAAAACGGCACTCGATTATGTTAA 472
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 473 CAGTTATTGGAACGAAAAAGGCATTGGATGTGGGAGGGAGAGTGTGTGACTGACCTCAA 532
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 467 CAGTTATTGGGCGCAAAATGGCATCGGATCGGGAGGGAGAGTGTGTACTGATCTGAA 526
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 CTCAACCGCCTTGGGGCTTCGAACCTCTCCGACTACACGGATACACTGTGTCTTCAGATGT 592
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 527 CTCAACTCGTTGGGGCTTCGAACCTACGACTACACGGATACCCGGTGTCTTCAGATGT 586
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTCCCTCCAATGCCAATATTCAGATAGA 652
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QY 587 TTTCAAAGCTTTCAAAGGCCAAAAATGGGCAGTTTTCCTGCTCTGAAAAATATTCAGACAGA 646
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QY 653 GGGAGAGATTAGAGCGGTTCTCAATTTATTAGGGCCCTCCCTCGTCGCCCTTCCCGCGGA 712
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QY 647 TGAAGAGATCAGAGCGGTTCTGAAATTTATCCGGCCCTCCCTCATTTGCGCTTCCAGGGGA 706
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 713 GAAAGTTATGGAAGCTGAAACATTTCTACAAAAATATTTAAGAGAGAGCCCTGCAAAA 772
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 707 GAAAAATTATGGATGAGGCTGAAATCTTCTCTACCAAATATTTTAAAGAGAGCCCTGCAAAA 766
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QY 773 GATTCGGGCATCCAGTATACTTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA 832
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Db 1124 TCTTATCACGGTTCTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACT 1183
QY 1184 CTTACAGCGCAATTAAGAGATGGGATCCGTCGCGCATGGAATGCCCTTCCAGAATATAT 1243
Db 1184 CTTACAGCGCAATTAAGAGATGGGATCCGTCGCGCATGGAATGCCCTTCCAGAATATAT 1243
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Db 1244 GAAAGGAGTGTACATAGCGGTTTACGACACCCGTAATAATGAAATGGCTCGAGAGGCAGAGGA 1303
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Db 1304 GGCTCAAGGCCCGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTTC 1363
QY 1364 GTATATGCAGGAAGCAAAAGTGGATCGCCACTGCTGTTATCTGCCCAAGTTTGGAGGAGTACTT 1423
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QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACACTGCAACCCATCTTGACGTT 1483
Db 1424 CGAGAAATGGGAAAGTTAGCTGTGTCATCGCATATCCGCATTTGCAACCCATCTTGACAAT 1483
QY 1484 GGACATCCCTTTCTGATCACATCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
Db 1484 GGACATCCCTTTCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAACGA 1543
QY 1544 CTTGATATGATCATCTTTCGATTAAAGAGTGATACACGGTGCTACAAAGCAGACAGGGC 1603
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QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGAGAATTAATTTG 1723
Db 1664 GGAAGATGCTCTCGATCATATCAACGCCATGATCAGTGACGTAATCAAGGATTAATTTG 1723
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QY 1784 AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
Db 1784 CGCCAGAGCTTTCCATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA 1843
QY 1844 AACAAAGAGTTTGGTGATGAGAACCGTTCATTGAACCTGTGCCCTTTGTAAACACACTTCAA 1903
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 1844 AACGAAGAGTTGGTCACGAGAACCCCTCCTTGAATCTGTGCCCTTTGTAGCAACAGCTCAA 1903

QY 1904 ATCTACAATAATAACTGAGGATGCCCTATGGGTGTATATAGGGCACACAAAAATAATAT 1963

Db 1904 ATCTATGCCCTATGCTATGTCGGGTTAAATATATATGTGAAGGTAGCCGTTGGATGTAGA 1963

QY 1964 GGTGTGTTAGTAAAGCTGTAATTTTATGAAAAAATAAAAAAAAAAAAAAAAAAAAA 2013

Db 1964 GGATAAGTTTGTATATAATTTAATAAGTTGTAATTTAAAAAATAAAAAAAAAAAAA 2013

RESULT 3

US-09-903-012-19

; Sequence 19, Application US/09903012

; Patent No. US20020094557A1

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph

; APPLICANT: No. US20020094557A11, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/903,012

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: 09/398,395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/100,993

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 19

; LENGTH: 2018

; TYPE: DNA

; ORGANISM: Abies grandis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (6)...(1889)

; OTHER INFORMATION: pinene synthase

US-09-903-012-19

Query Match 64.9%; Score 1306.8; DB 9; Length 2018;

Best Local Similarity 81.0%; Pred. No. 0;

Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY 68 CAGGTGCTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT 127

Db 53 CAAATCGTTGATCAGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCT 112

QY 128 TGAATCTGCAGGCCGGGAAATCCGTCGGCATTCATTAACATGTGTTTGAACAGCGT 187

Db 113 AGGAATGAGTAGCGGAGGAAATCTATCACTCTTCATCAGCATGAGCTCTACCCCGT 172

QY 188 CGCATCTACTGATTTCTGACAGAGACGCGTGGGCAACTATCATTCCAACTGTGGGACGA 247

Db 173 TGTAACCGATGATGGTGTACGAAGACGCGATGGCGGATTTCCATTCCAACTCTGGGACGA 232

QY 248 TGATTTTACATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGGAACTGC 307

Db 233 TGATGTCATACAGTCT---TTACCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGC 289

QY 308 TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAAATTTCAAGTCGCTGGAAGATGG 367

Db 290 TGAGAACTGATCGGGGAAGTAAAG--AACATGTTCAATTCGATGTCATTAGAAGATGG 346

QY 368 AG-----GCAATGATCTCCTTCAACGACTTTTGTGGTCGATGACGTTGA 412

Db 347 AGAGTTAATGAGTCCGCTCAATGATCTCATTCAACGCCCTTTGGATTGTTCGACAGCCCTGA 406

QY 413 ACGTTGGGAATCGACAGGCGATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTAA 472

Db 407 ACGTTTGGGATCCATAGACATTTCAAAGATGAGATAAAATCGGCGTTGATTATGTTTA 466

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QY 1244 GAAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA 1303

Db 1244 GAAAGGAGTGTACATAGCGGTTTACGACACCCGTAATGAAATGGCTCGAGAGGAGAGGA 1303

QY 1304 GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGAGGCTTGGAGGCGTGTGTTGATTC 1363

Db 1304 GGCTCAAGGCCGAGATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATTGATTC 1363

QY 1364 GTATATGCAGGAAGCAAAAGTGGATCGCCACTGGTTATCTGCCACCGTTTGAGGAGTACTT 1423

Db 1364 GTATATGCAAGAAAGCAAGTGGATCGCCACTGGTTACTCTGCCCTCCTTTGATGAGTACTA 1423

QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCTTGCACACTGCGCACTGCAACCCATTCTGACGTT 1483

Db 1424 CGAGAATGGGAAAGTTAGCTGTGGTCATCGCATATCCGCATTCGCACTTGCAACCCATTCTGCAAT 1483

QY 1484 GGACATCCCTTTTCTGATCACATCTCTCAAGGAAAGTTGACTTCCCATCGAAGCTCAATGA 1543

Db 1484 GGACATCCCCCTTTCCCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAACGA 1543

QY 1544 CTTGATATGATCATCTTCGATTAAAGAGGTGATACACGGTGCTACAAGGACAGACAGGGC 1603

Db 1544 CTTGGCATGTGCCATCCTTCGATTACGAGGTGATACGGGTGCTACAAGGCGACAGGGC 1603

QY 1604 CCGTGGAGAAGAAGCTTCGTCTATATCATGTTATATGAAGACAATCCTGGATTAAACGGA 1663

Db 1604 TCGTGGAGAAGAAGCTTCCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGA 1663

QY 1664 AGAAGATGCTCTGAATCATATCAACTTCANGATCAGGGACGCAATCAGAGAAATTAATG 1723

Db 1664 GGAAGATGCTCTCGATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAATG 1723

QY 1724 GGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCACTTCCAAGAAACACGCAATTTGACAT 1783

Db 1724 GGAACCTTCTCAAACACAGACATCAATGTTCCCATCTCGCGAAGAAACATGCTTTTGACAT 1783

QY 1784 AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843

Db 1784 CGCCAGAGCTTTCCATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA 1843

QY 1844 AACAAAGAGTTTGGTGATGAGAACCGTCAATTGAACCTGTGCCTTTGTAAACAACACTTCAA 1903

Db 1844 AACGAAGAGTTTGGTCAGAGAACCCCTCCTTGAATCTGTGCCCTTTGTAGCAACAGCTCAA 1903

QY 1904 ATCTACAATATTAACTGAGGATGCCCTATAGGTGTATATAGGCGACACAAAAATAAATAT 1963

Db 1904 ATCTATGCCCTATGCTATGTCCGGTTAAATAATATATGTGAAGGTAGCCGTTGGATGTAGA 1963

QY 1964 GGTGTGTTAGTAAAGCTGTAATTTATGAAAAAATAAAAAAAAAAAAAA 2013

Db 1964 GGATAAGTTTGTATAAATTTAATAAAGTTGTAATTTAAAAAATAAAAAAAAAAAAAA 2013

RESULT 4

US-09-900-797-19

; Sequence 19, Application US/09900797  
; Publication No. US20030087406A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20030087406A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/900,797  
; CURRENT FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: US/09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 2018  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)...(1889)  
; OTHER INFORMATION: pinene synthase

US-09-900-797-19

Query Match 64.9%; Score 1306.8; DB 10; Length 2018;  
Best Local Similarity 81.0%; Pred. No. 0;  
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY 68 CAGTGTGCTCAGTCTCTCTCATGAGATTAAAGGCTCTCCGTTAGAACAAATCCCAACTCT 127

Db 53 CAAATCGTTGATCAGTTCTACCCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCT 112

QY 128 TGAATCTGCAGCCCGGGGAAATCCGTCCGGCATTCATAAACATGTGTTTGACAAGCGT 187

Db 113 AGGAATGAGTAGGCGAGGGAATCTATCACTCCTCCATCAGCATGAGCTCTACACCGT 172

QY 188 CGCATCTACTGATTCTGTACAGAGACGCGTGGGCAACTATCATTCCAACCTGTGGACGA 247

Db 173 TGTAAACCGATGATGTTGTACGAAGACGCGATGGCGGATTTCCATTCCAACCTCTGGACGA 232

QY 248 TGATTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGAAACGTGC 307

Db 233 TGATGTCTACAGTCT--TTACCAACCGCTTATGAGGAAAAATCGTACCTCGAGCGTGC 289

QY 308 TGACAGACTTATTTGGGAAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG 367

Db 290 TGAGAAACTGATCGGGGAAGTAAAG--AACATGTTCAATTCGATGTCATTAGAAGATGG 346

QY 368 AG-----GCAATGATCTCCTTCAACGACTTTTGTGCTGGTCGATGACGTTGA 412

Db 347 AGAGTTAATGATCCGCTCAATGATCTCATTCAAAGCCTTTGGATTGTCGACAGCCTTGA 406

QY 413 ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAA 472

Db 407 ACGTTTGGGATCCATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATGTTA 466

QY 473 CAGTTATTGGAACGAAAAAGGCAATTGGATGCGGAGGGAGAGTGTGTGACTGACCTCAA 532

Db 467 CAGTTATTGGGCGAAAAATGGCATCGGATCGGGAGGGAGAGTGTGTTACTGATCTGAA 526

QY 533 CTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT 592

Db 527 CTCAACTGCGTTGGGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGT 586

QY 593 TTTGAACGTTTTTAAAGACAAAAATGGCAATTTTCTCCACTGCCAATAATTGAGATAGA 652

Db 587 TTTCAAAGCTTTCAAAGGCCAAATGGCAGTTTCTGCTCTGAAAAATATTCAGACAGA 646

QY 653 GGGAGAGATTAGAGGCGTTCTCAATTTATTCAGGGCCTCCCTCGTCGCCCTTTCCCGGCGA 712

Db 647 TGAAGAGATCAGAGGCGTTCTGAATTTATTCGGGGCCTCCCTCATTCGCTTTCCAGGGGA 706

QY 713 GAAAGTTATGGATGAAGCTGAAACATCTCTACAAAAATATTTAAGAGAAAGCCCTGCAAAA 772

Db 707 GAAATTTATGGATGAGGCTGAAATCTTCTACCAAAATATTTAAAGAAAGCCCTGCAAAA 766

QY 773 GATTCGGGCATCCAGTATACCTTCTACAGAGATACGGACGTTCTGGAATATGTTGGCA 832

Db 767 GATTCGGGCTCCAGT---CTTTCGCGAGAGATCGGGGACGTTTTTGGAAATATGTTGGCA 823

QY 833 CACCAATTTGCCACGCTTGGAAAGCAAGGAATTACATGGACGTCCTTTGGACAGCACACTAA 892

Db 824 CACATATTTGCCGCGATTGGAAGCAAGGAATTACATCCAAGTCTTTGGACAGGACACTGA 883

QY 893 AAATAAGAACGC-----CGCCGAGAAAACTTTTAGAACCTTGCAAAATTTGGAATTCAA 943

Db 884 GAACACGAAGTCATATGTGAAGAGCAAAAAAATTTTAGAACCTCGCAAAATTTGGAGTTCAA 943

QY 944 TATATTTCACTCCTTACAAGAGAGAGAGTTAAACATGTTTCCCGATGGTGGAAAGACTC 1003

Db 944 CATCTTTCAATCCTTACAAAAGAGGGAGTTAGAAAGTCTGGTCAGATGGTGGAAAGATC 1003

QY 1004 GGGTTCTCCTGAGATGACCTTCTGTCTGACATCGTCACGTGGAATACTACGCTTTGGCTTC 1063

Db 1004 GGGTTTCTCTGAGATGACCTTCTGCGACATCGTCACGTGGAAATACTACACTTTGGCTTC 1063

QY 1064 CTGCATTCGTTTCGAGCCTCAACATTTCTGGATTTCAGACTCGGCTTTACCAAGATGTCTCA 1123

Db 1064 CTGCATTCGTTTCGAGCCTCAACATTTCTGGATTTCAGACTCGGCTTTGCCAAGACGTGTCA 1123

QY 1124 TCTTATCACGGTTCTTTGACGACATGTACGACGCTTTCGSCACAGTAGACGAGCTGGAAC 1183

Db 1124 TCTTATCACGGTTCTTTGACGATATGTACGACACCTTTCGGCACAGTAGACGAGCTGGAAC 1183



QY 1184 CTTACAGCGACAATTAAGAGATGGATCCGTCCGCGATGGAATGCCCTCCAGAAATATAT 1243  
Db |||||  
QY 1184 CTTACAGCGACAATGAAGAGATGGATCCGTCCGATAGATTGCCCTCCAGAAATATAT 1243  
Db |||||  
QY 1244 GAAAGGAGTACATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA 1303  
Db |||||  
QY 1244 GAAAGGAGTACATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCAGAGGA 1303  
Db |||||  
QY 1304 GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTTTTGATTC 1363  
Db |||||  
QY 1304 GGCTCAAGGCCGAGATACGCTCACATATGCTCGGAAGCTTGGGAGGCTATATTGATTC 1363  
Db |||||  
QY 1364 GTATATGCAAGAACGAAAGTGATGCGCACTGGTTATCTGCCACGCTTGGAGGAGTACTT 1423  
Db |||||  
QY 1364 GTATATGCAAGAACGAAAGTGATGCGCACTGGTTACCTGCCCTCCTTTGATGAGTACTA 1423  
Db |||||  
QY 1424 GGAGAACGGGAAAGTTAGTCTGTCTCATCGCCCATGCGCACTGCAACCCATCTGACGTT 1483  
Db |||||  
QY 1424 CGAGAAATGGGAAAGTTAGTCTGTGTCTATCGCATATCCGCATTTGCAACCCATCTGACAAT 1483  
Db |||||  
QY 1484 GGACATCCCTTTCTCTGATCACATCCTCAAGAAAGTTGACTTCCCATCGAAAGCTCAATGA 1543  
Db |||||  
QY 1484 GGACATCCCTTTCTCTGATCATATCCTCAAGAAAGTTGACTTCCCATCAAGAGCTTAAACGA 1543  
Db |||||  
QY 1544 CTTGATATGATCATCCTTCGATTAAAGAGGTGATACACGGTGCTACAAAGCAGACAGGGC 1603  
Db |||||  
QY 1544 CTTGGCATGTGCCATCCTTCGATTACGAGGTGATACGGGTGCTACAAAGCGGACAGGGC 1603  
Db |||||  
QY 1604 CCGTGGAGAAAGAGCTTCGTCTATATCATGTTATATGAAAGACAATCCTGGATTAAACGGA 1663  
Db |||||  
QY 1604 TCGTGGAGAAAGAGCTTCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGA 1663  
Db |||||  
QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGAGAAATTAATTG 1723  
Db |||||  
QY 1664 GGAAGATGCTCTCGATCATATCAACGCCATGATCAGTGACGTAATCAAGGATTAATTG 1723  
Db |||||  
QY 1724 GGAGCTTCTAAAGCCAGACAAACAGTGTTCCTATCACTTCCAAGAAACACGCAATTTGACAT 1783  
Db |||||  
QY 1724 GGAACCTTCTCAACCCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACAT 1783  
Db |||||  
QY 1784 AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843  
Db |||||  
QY 1784 CGCCAGAGCTTTCCTATACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA 1843  
Db |||||  
QY 1844 AACAAAGAGTTTGGTATGAGAACCGTCAATTGAACCTGTGCCTTTGTAAACACACTTCAA 1903  
Db |||||  
QY 1844 AACGAAGAGTTTGGTACAGAACCTTCCCTTGAATCTGTGCCTTTGTAGCAACAGCTCAA 1903  
Db |||||  
QY 1904 ATCTACAATATTAAGTACGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 1963  
Db |||||  
QY 1904 ATCTATGCCCTATGCTATGTGCGGTTAAATATATATGTTGAAGGTAGCCGTTGGATGTAGA 1963  
Db |||||  
QY 1964 GGTGTGTTAGTAAGCTGTAATTTATGAAAAAATAAATAAATAAATAAATAAATAAATAA 2013  
Db |||||

RESULT 5  
US-09-893-820-19  
; Sequence 19, Application US/09893820  
; Publication No. US20040053386A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20040053386A1, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/893,820  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US/09/398,395A  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,993

; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 2018  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)...(1889)  
; OTHER INFORMATION: pinene synthase  
US-09-893-820-19  
  
Query Match 64.9%; Score 1306.8; DB 13; Length 2018;  
Best Local Similarity 81.0%; Pred. No. 0;  
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;  
  
QY 68 CAGGTCGTGCCTCAGTCTCTTCTCATGAGATTAAGGCTCTCCGTTAGAACAAATCCCAACTCT 127  
Db |||||  
QY 53 CAAATCGTTGATCAGTCTTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCT 112  
Db |||||  
QY 128 TGGAAATCTGCAGCCGGGGGAAATCCGTCGGCATTCATATAAACATGTGTTTGACAAGCGT 187  
Db |||||  
QY 113 AGGAATGATAGGCGAGGGAAATCTATCACTCTTCCATCAGCATGAGCTTACCACCGT 172  
Db |||||  
QY 188 CGCATCTACTGATTTCTGTACAGAGACGGCTGGGCAACTATCATTTCCAACCTGTGGACGA 247  
Db |||||  
QY 173 TGTAAACCGATGATGGTGTACGAAGACGCAATGGGCGATTTCCATTTCCAACCTGTGGACGA 232  
Db |||||  
QY 248 TGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGGAACGTCG 307  
Db |||||  
QY 233 TGATGTCTATACAGTCT---TTACCAACGGCTTATGAGGAAAAATCGTACTGGAGCGTGC 289  
Db |||||  
QY 308 TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGTCGGAAGATGG 367  
Db |||||  
QY 290 TGAGAAACTGATCGGGGAAGTAAAG---AACATGTTCAATTCGATGTCATTAAGATGG 346  
Db |||||  
QY 368 AG-----GCAATGATCTCCTTCAACGACTTTTGTGTCGATGACGTTGA 412  
Db |||||  
QY 347 AGAGTTAATGATCGGCTCAATGATCTCATTTCAACGCTTTTGGATTTGCGACAGCCTTGA 406  
Db |||||  
QY 413 ACCTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCCTCGATATGTTAA 472  
Db |||||  
QY 407 ACCTTTGGGGATCCATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATATGTTA 466  
Db |||||  
QY 473 CAGTTATTGGAACGAAAAAGGCATTTGGATGTGGAGGGAGAGTGTGTTGACTGACCTCAA 532  
Db |||||  
QY 467 CAGTTATTGGGCGAAAAATGGCATCGGATCGGAGGGAGAGTGTGTTTACTGATCTGAA 526  
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QY 533 CTCAACCGCCTTGGGCTTCGAACCTCTCCGACTACACGGATACACTGTGTCTTCAGATGT 592  
Db |||||  
QY 527 CTCAACTGCGTTGGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGT 586  
Db |||||  
QY 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATTCAGATAGA 652  
Db |||||  
QY 587 TTTCAAAGCTTTCAAAGGCCAAAAATGGGCAAGTTTCTGCTCTGAAAAATATTCAGACAGA 646  
Db |||||  
QY 653 GGGAGAGATTAGAGGCTTCTCAATTTATTCAGGGGCTCCCTCGTCGCCCTTCCGGCGGA 712  
Db |||||  
QY 647 TGAAGAGATCAGAGGCTTCTGAATTTATTCGGGCTCCCTCATTTGCCCTTCCAGGGGA 706  
Db |||||  
QY 713 GAAAGTTATGGATGAAGCTGAAACATTTCTCTACAAAAATTTAAAGAGAAAGCCCTGCAAAA 772  
Db |||||  
QY 707 GAAATATGGATGAGGCTGAAATCTTCTCTACCAAAATATTAAAGAAAGCCCTGCAAAA 766  
Db |||||  
QY 773 GATTCCGGCATCCAGTATACCTTTCAGTACAGATACGGGACGTTCTTGGAAATATGTTGGCA 832  
Db |||||  
QY 767 GATTCCGGTCTCCAGT---CTTTCGGGAGAGATCGGGGACGTTTGGAAATATGTTGGCA 823  
Db |||||



QY	833	CACCAAA	TTGCCAC	GCCTTGG	AAGCAAG	GAATTACA	TGGAC	GTCTTTGG	ACAGCAC	TA	892
Db	824	CACATA	TTGCCG	GATTGGA	AGCAAG	GAATTACA	TCCAA	GTCTTTGG	ACAGCAC	TGA	883
QY	893	AAATAA	GAAACG	-----	CGCCG	AGAAA	CACTTT	TAGAA	CTTGCA	AAAT	943
Db	884	GAAACG	AAAGT	TCATAT	GTGA	AGACAAA	AAACCTTT	TAGAA	CTCGCA	AAAT	943
QY	944	TATAT	TTCACT	CCCTTACA	AGAGAG	AGATTAA	AAACATGTTT	CCCGAT	GGTGGA	AAAGACTC	1003
Db	944	CATCT	TTCAAT	CCCTTACA	AAAGAG	GGAGTTAG	AAAGTCTG	GTTCAG	ATGGTGGA	AAAGATC	1003
QY	1004	GGGTT	CTCTG	AGATGAC	CTTCTGT	CGACATCGT	CACGTG	GAATACTAC	CGTTTGG	CTTC	1063
Db	1004	GGGTT	TTCTG	AGATGAC	CTTCTG	CGACATCGT	CACGTG	GAATACTAC	CACTTTGG	CTTC	1063
QY	1064	CTGCAT	TGCGT	TCGAGC	CTCAAC	ATTCTGG	ATTCAG	ACTCGG	CTTTAC	CAAGATG	1123
Db	1064	CTGCAT	TGCGT	TCGAGC	CTCAAC	ATTCTGG	ATTCTG	GAATCTG	CAAGAC	GTGTCA	1123
QY	1124	TCTTAT	CACGGT	CTTGTAC	GACATGTAC	GACGTCTT	CGGCAC	AGTAGAC	GCAGCTG	GAACT	1183
Db	1124	TCTTAT	CACGGT	CTTGTAC	GACATGTAC	GACACCTT	CGGCAC	AGTAGAC	GCAGCTG	GAACT	1183
QY	1184	CTTCA	CAGCGA	CAATTA	AGAGAT	GGGATCCG	TCCGCG	ATGGAATGC	CTTCC	CAGAA	1243
Db	1184	CTTCA	CAGCGA	CAATTA	AGAGAT	GGGATCCG	TCCGCG	ATGGAATGC	CTTCC	CAGAA	1243
QY	1244	GAAAG	GAGTGTAC	ATGATG	GTGTTTAT	CACAC	CCGTAATG	AAATGG	CTCGAG	TGGCAG	1303
Db	1244	GAAAG	GAGTGTAC	ATGATG	GTGTTTAT	CACAC	CCGTAATG	AAATGG	CTCGAG	TGGCAG	1303
QY	1304	GGCTC	AAAGCCG	AGACAC	CGCTCA	ACTATG	CAAGAC	AGCAGCTT	GGAGG	CGTGT	1363
Db	1304	GGCTC	AAAGCCG	AGATAC	CGCTCA	CATATG	CTCGG	AAAGCTTGG	GAGGCTT	ATATTG	1363
QY	1364	GTATAT	GCAGGA	AGCAAGT	TGATCG	CCACTG	GTGTTAT	TCTG	CCCCAC	GTTTGAG	1423
Db	1364	GTATAT	GCAGGA	AGCAAGT	TGATCG	CCACTG	GTGTTAT	TCTG	CCCCAC	GTTTGAG	1423
QY	1424	GGAGA	ACGGG	AAAGTTAG	CTGTCT	GCTCAT	CGCCCAT	GCGCA	CTGCA	ACCCATT	1483
Db	1424	CGAGA	ATGGG	AAAGTTAG	CTGTCT	GCTCAT	CGCATAT	CCGCAT	TGCA	ACCCATT	1483
QY	1484	GGACAT	CCCCCT	TTCC	TGATC	ACATCC	CTCAAG	GAAGTTGACTT	CCCAT	CGAAGCT	1543

Db 1904 ATCTATGCCCTATGCTATGTCTGGGTTAAAAATATATGTGGAAGGTAGCCGTTGGATCTAGA 1963  
 QY 1964 GGTGTGTAGTAAAGCTGTAATTTATGAAAAAATAAAAAAAAAAAAAA 2013  
 Db 1964 GGATAAGTTTGTATAAATTTAATAAAGTTGTAATTTAAAAAATAAAAAAAAAA 2013

RESULT 6  
 US-10-041-007-21  
 ; Sequence 21, Application US/10041007  
 ; Publication No. US20020164736A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Matsuda, Seiichi P.T.  
 ; APPLICANT: Schepmann, Hala G  
 ; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase  
 ; FILE REFERENCE: P02081US1  
 ; CURRENT APPLICATION NUMBER: US/10/041,007  
 ; CURRENT FILING DATE: 2002-01-07  
 ; PRIOR APPLICATION NUMBER: US 60/259,881  
 ; PRIOR FILING DATE: 2001-01-05  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 21  
 ; LENGTH: 2018  
 ; TYPE: DNA  
 ; ORGANISM: Abies grandis  
 US-10-041-007-21

	Query Match	64.9%;	Score 1306.8;	DB 14;	Length 2018;
	Best Local Similarity	81.0%;	Pred. No. 0;		
	Matches 1595;	Conservative	0;	Mismatches 342;	Indels 33; Gaps 5;
QY	68	CAGGTCGTCCTCAGTCTCTTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCCCAACTCT	127		
Db	53	CAAAATCGTTGATCAGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCT	112		
QY	128	TGGAATCTCAGGCCGGGGAATCCGTCGCGCATTCATATAACATGTGTTGACAAGCGT	187		
Db	113	AGGAATGAGTAGGGGAGGGAATCTATCACTCTTCCATCAGCATGAGCTCTACCACCGT	172		
QY	188	CGCATCTACTGATTTCTGTACAGAGACGCGTGGGCAACTATCATCCAACTGTGGGACGA	247		
Db	173	TGTAACCGATGATGGTGTACGAAGACGCGATGGGCGATTTCCATTCCAACCTCTGGGACGA	232		
QY	248	TGATTTCTATACAGTCTCTGTATCTCAACGCCCTTATGGAGCACCTGATTACGGGAACGTGC	307		
Db	233	TGATGTCATACAGTCT---TTACCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGC	289		
QY	308	TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG	367		
Db	290	TGAGAACTGATCGGGGAAGTAAAG---AACATGTTCAATTCGATGTCATTAGAAGATGG	346		
QY	368	AG-----GCAATGATCTCTTCAACGACTTTTTCGTCGTCGATGACGTTGA	412		
Db	347	AGAGTTAATGAGTCGCTCAATGTATCTCATTTCAACGCCCTTTGGATTGTCGACAGCCTTGA	406		
QY	413	ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAA	472		
Db	407	ACGTTTGGGGATCCATAGACATTTCAAAGATGAGATAAAAAATCGGCGCTTGATTATGTTTA	466		
QY	473	CAGTTATGGAAACGAAAAAGCAATTCGATGTGGGAGGGAGAGTGTGTGACTGACCTCAA	532		
Db	467	CAGTTATGGGGCGAAAAATGGCATCGGATCGGGAGGGAGAGTGTGTACTGATCTGAA	526		
QY	533	CTCAACCGCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT	592		
Db	527	CTCAACTCGTGTGGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGT	586		
QY	593	TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCTCCACTGCCAATATTCAGATAGA	652		
Db	587	TTTCAAAGCTTTCAAAGGCCAAATGGGCAGTTTTTCTGCTGTGAAAAATATTCAGACAGA	646		

QY	653	GGGAGAGATTAGAGCGGTTCTCTCAATTTATTCAGGGCCTCCCTCGTCGCCCTTTC	CGGCGA	712
Db	647	TGAAGAGATCAGAGCGGTTCTGAATTTATTCGGGCCCTCCCTCATTTGCCCTTCCAGGGGA	706	
QY	713	GAAAGTTATGGATGAAGCTGAAACATTTCTCTACAAAAATATTTAAGAGAAAGCCCTGCAAAA	772	
Db	707	GAAAAATTATGGATGAGGCTGAAATCTTTCTCTACCAAAATATTTAAAAGAAAGCCCTGCAAAA	766	
QY	773	GATTCGGGCATCCAGTATACCTTTTCACTAGAGATACGGGACGTTCTTGGAAATATGGTTGGCA	832	
Db	767	GATTCGGGCTCCAGT--CTTTCCGAGAGATCGGGGACGTTTTTGGAAATATGGTTGGCA	823	
QY	833	CACCAATTTGCCACGCTTGGAAAGCAAGGAATTACATGGACGTCCTTTGGACAGCACACTAA	892	
Db	824	CACATATTTGCCGCGATTGGAAGCAAGGAATTACATCCAAGTCCTTTGGACAGGACACTGA	883	
QY	893	AAATAAGAACGC-----CGCCGAGAAACCTTTTAGAACTTGCAAAAATTGGAATTCAA	943	
Db	884	GAACACGAAAGTCATATGTGAAGAGCAAAAAACCTTTTAGAACTCGCAAAATTTGGAGTTCAA	943	
QY	944	TATATTTCACTCCTTACAAGAGAGAGAGTTAAAAACATGTTTCCCGATGGTGGAAGACTC	1003	
Db	944	CATCTTTCAATCCTTACAAAGAGGGAGTTAGAAAGTCTGGTCAGATGGTGGAAGAAATC	1003	
QY	1004	GGGTTCTCCTGAGATGACCTTCTGTGACATCGTCACTGGAAATACTACGCTTTTGGCTTC	1063	
Db	1004	GGGTTTTCTGAGATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTTGGCTTC	1063	
QY	1064	CTGCATTCGGTTTCAGACCTCAACATTTCTGGATTCAGACTCGGCTTTACCAAGATGTCTCA	1123	
Db	1064	CTGCATTCGGTTTCAGACCTCAACATTTCTGGATTCAGACTCGGCTTTGCCAAGACGTTCA	1123	
QY	1124	TCTTATCACGGTTCTTGACGACATGTACGACGTCCTTCGGCACAGTAGACGAGCTGGAAC	1183	
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QY	1184	CTTCACAGCGACAATTAAAGAGATGGATCCGTCGGGATGGAATGCCTTCAGAAATATAT	1243	
Db	1184	CTTCACAGCGACAATTAAAGAGATGGATCCGTCGGGATGGAATGCCTTCAGAAATATAT	1243	
QY	1244	GAAAGGAGTGTACATGAGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA	1303	
Db	1244	GAAAGGAGTGTACATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCGAGAG	1303	
QY	1304	GGCTCAAGCGCGAGACAGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTTTTGATTC	1363	
Db	1304	GGCTCAAGCGCGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTC	1363	
QY	1364	GTATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAGGAGTACTT	1423	
Db	1364	GTATATGCAGGAAGCAAGTGGATCGCCACTGGTTACCTGCCCTCCTTTGATGAGTACTA	1423	
QY	1424	GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATCGGCACTGCAACCCCATTTCTGACGTT	1483	
Db	1424	CGAGAAATGGGAAAGTTAGCTGTGGTTCATCGCATATCCGCAATGCAACCCCATTTCTGACAA	1483	
QY	1484	GGACATCCCCTTTCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA	1543	
Db	1484	GGACATCCCCTTTCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCTTAAACGA	1543	
QY	1544	CTTGATATGTATCATCCTTCGATTAGAGGTGATACACGGTGTCTACAAGGCGACAGGCG	1603	
Db	1544	CTTGCCATGTGCCATCCTTCGATTACGAGGTGATACCGCGTGTCTACAAGGCGACAGGCG	1603	
QY	1604	CCGTGGAGAAAGCTTCGTCATATCATGTTTATATGAAGACAATCCTGGATTAAACGGA	1663	
Db	1604	TCGTGGAGAAAGCTTCCTCTATATCATGTTTATATGAAGACAATCCTGGAGTATCAGA	1663	
QY	1664	AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGAGAATTAATTG	1723	
Db	1664	GGAGATGCTCTCGATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAAATTG	1723	
QY	1724	GGAGCTTCTAAAGCCGAGACAACAGTGTTCCTCATCCTTCCAAGAAACACGCAATTTGACAT	1783	

## RESULT 7

US-10-025-145A-3

: Sequence 3. Application US/10025145A

Publication No. US20030175861A1

: GENERAL INFORMATION:

GENERAL INFORMATION: APPLICANT: Croteau Rodney B.

APPLICANT: CROCEAU, RODNEY  
APPLICANT: BOHLMANN, JOERG

APPLICANT: BOHLMANN, JOSEPH  
APPLICANT: STEELE CHRISTOPHER L.

APPLICANT: PHILLIPS MICHAEL A  
APPLICANT: STEELE, CHRISTOPHER

APPLICANT: PHILLIPS, MICHAEL A.  
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (*Abies Grandis*)

;; TITLE OF INVENTION: MOHOLE  
FIVE REFERENCE: WCIB118414

FILE REFERENCE: WSUR118414  
CURRENT ADDITION NUMBER: USC/10/025 1458

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; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: PCT

; PRIOR FILING DATE: 1998-07-10

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 1997-0

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: I

; SEQ ID NO 3

; LENGTH: 20

; TYPE: DNA

ORGANISM

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;
FEATURE:

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; NAME/KEY: CDS

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LOCATION: (6) .. {18
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OTHER INFORMATION

Query Match 64.9%; Score 1306.8; DB 15; Length 2018;  
Best Local Similarity 81.0%; Pred. No. 0;  
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY	68	CAGGTCGTCCCTCAGTTCCTCTCATGAGATTAAGGCTCTCCGTAGAA	127	CAATCCCAACTCT	127
Db	53	CAAAATCGTTGATCAGTTCCTACCCATGAGCTTAAGGCTCTCTTAGAA	112	CAATTCGAGCTCT	112
QY	128	TGGAATCTGCAGGCCGGGAAATCCGTCGCGCATTCATATAA	187	CATGTGTTTGACAAGCGT	187
Db	113	AGGAATGAGTAGGCGAGGGAATCTATCACTCCTTCCATCAGCATGAGCTCTACCA	172	CCCGT	172
QY	188	CGCATCTACTGATTCCTGTACAGAGACGCGTGGGCAACTATCAT	247	TCCAACTGTGGGACGA	247
Db	173	TGTAACCGATGATGGTGTACGAAGACGCATGGGCGATTTC	232	CAACTCTGGGACGA	232
QY	248	TGATTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGAT	307	TACGGGAAACGTGC	307
Db	233	TGATGTCATACAGTCT---TTACCAACGGCTTATGAGGAAAAATCGT	289	TACCTGGAGCGTGC	289
QY	308	TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAATTTCAAGT	367	TCGCTGGAAGATGG	367

Db 290 TGAGAAACTGATCGGGGAAGTAAAG---AACATGTTCAATTCGATGTCATTAGAAGATGG 346

QY 368 AG-----GCAATGATCTCCTTCAACGACTTTTGTGCTGGTCGATGACGTTGA 412

Db 347 AGAGTTAATGAGTCGCTCAATGATCTCAITCAACGCCTTTGGATTGTCGACAGCCTTGA 406

QY 413 ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGAATATGTTAA 472

Db 407 ACGTTTGGGATCCATAGACATTTCAAAGATGAGATAAAAATCGGCGCTTGATATGTTTA 466

QY 473 CAGTTATTGGAACGAAAAAGGCATTTGGATGTGGAGGGAGAGTGTGTGACTGACCTCAA 532

Db 467 CAGTTATTGGGGCAAAAATGGCATCGGATCGGGAGGGAGAGTGTGTGTTACTGATCTGAA 526

QY 533 CTCAACCGCCTTGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT 592

Db 527 CTCAACTCGTTGGGCTTCGAACCTTACGACTACACGGATACCCGGTGTCTTCAGATGT 586

QY 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCTCCACTGCCAATATTCAGATAGA 652

Db 587 TTTCAAAGCTTTCAAAGGCCAAAATGGGCAGTTTTCTGTCTGTAATAATTCAGACAGA 646

QY 653 GGGAGAGATTAGAGCGGTTCTCAATTTATTAGGGCCTCCCTCGTGCCTTTCCCGCGA 712

Db 647 TGAAGAGATCAGAGCGGTTCTGAATTTATTCCGGGCCTCCCTCATTTGCCTTTCCAGGGGA 706

QY 713 GAAAGTTATGATGAAGCTGAAACATTTCTACAAAAATATTTAAGAGAGAGCCCTGCAAAA 772

Db 707 GAAATTTATGGATGAGGCTGAAATCTTCTACCAAATATTTAAAGAAAGCCCTGCAAAA 766

QY 773 GATTCCGGCATCAGATATACTTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA 832

Db 767 GATTCCGGTCTCCAGT---CTTTCGGGAGAGATCGGGACGTTTGGTAATATGTTGGCA 823

QY 833 CACCAATTTGCCACGCTTGGAGCAAGGAATTACATGGACGCTCTTTGGACAGCACACTAA 892

Db 824 CACATATTTGCCGCGATTGGAAGCAAGGAATTACATCCAAGTCTTTTGGACAGGACACTGA 883

QY 893 AAATAAGAACGC-----CGCCGAGAAACTTTTAGAACTTGCAAAATTTGGAATTCAA 943

Db 884 GAACACGAAGTCATATGTGAAGAGCAAAAACACTTTTAGAACTCGCAAAATTTGGAGTTCAA 943

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QY 1184 CTTCAAGCGACAATTAAGAGATGGGATCCGTCGGCGATGGAATGCCTTCCAGAAATATAT 1243

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Db 1304 GGCTAAGCGGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTC 1363

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RESULT 8

US-10-025-145A-77  
; Sequence 77, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUP118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77  
; LENGTH: 1890  
; TYPE: DNA  
; ORGANISM: Abies Grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1890)  
; OTHER INFORMATION:  
US-10-025-145A-77



Query Match		54.3%;	Score 1092.4;	DB 15;	Length 1890;
Best Local Similarity		76.8%;	Pred. No..8.6e-313;		
Matches 1439;		Conservative	0;	Mismatches 396;	Indels 39; Gaps 7;
QY	46	TTTCTATTACTCCGCTGGTTTCCAGGTCGTCGCTCAGTCTCTTCTCATGAGATTAAGGCTC	105		
Db	26	TGTCCTCCAAATCGGCTCTGCACAAATCGTGGATCGTTTCTACTTATGAGCATAAAGGCTA	85		
QY	106	TCCGTAGAACAAATCCCAACTCTTGGAAATCGCAGGCCGGGAAATCCGTCGCGCATTTCCA	165		
Db	86	TCAGTAGAACAAATCCCAATCTTGGATTGCGTGGCGAGGAAATCTGTACACATTTCCC	145		
QY	166	TAAACATGTGTTTGACAAAGCGTCGCATCTACTG---ATTCTGTACAGACGCGTGGGCA	222		
Db	146	TGAGAAATGAGTTTGAGCACCGCAGTCTCTGATGATCATGGTGTACAAAGACGCATAGTCG	205		
QY	223	ACTATCATTCCAACCTGTGGACGATGATTTCATACAGTCTCTGATCTCAACGCCCTTATG	282		
Db	206	AGTTTCAATCCCAATCTGTGGACGACGATTTTATACAATCTC---TATCAACGCCCTTATG	262		
QY	283	GAGCACCTGATTACCGGGAACGTGCTGACAGACTTATTGGGGAAGTAAAGGATATAATGT	342		
Db	263	GGGCACCTTCATACCGTGAACGTGCTGATAGACTTATTGTGGAAGTAAAGGATATA--T	319		
QY	343	TCAATTTCAAGTCGCTGGAAGATGGAG-----GCAATGATCTCCTTCAAC	387		
Db	320	TCACTTCAATTTAGCGGAAGATGGAGAACTAATCACTCCCTCAATGATCTCATTTCAAC	379		
QY	388	GACTTTTGTGTCGATGACGTTTGAACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGA	447		
Db	380	GCCTTTTAAATGTCGATAACGTTGAACGTTTAGGATTTGATAGACATTTCAAAAAATGAGA	439		
QY	448	TAAAAACGGGCACTCGATTATGTTAAACAGTTATTGGAACGAAAAAGGCATTTGGATGGGA	507		
Db	440	TAAAAGCAGCACTAGACTATGTTTACAGTTATTGGAACGAAAAAGGCATTTGGCAGTGGAA	499		
QY	508	GGGAGAGTGTGTGACTGACCTCAACTCAACCGCCTTGGGCTTCGAACTCTCGACTAC	567		
Db	500	GTGATAGTGTGTGCTGATCTCAACTCAACTGCCCTGGGTTTCGAAATCTTCGACTAC	559		
QY	568	ACGGATACACTGTGTCTTCAGATGTTTGAACGTTTAAAGACAAAAATGGGCA---AT	624		
Db	560	ACGGATACAGTGTCTTTCAGATGTGTTGGAACACTTCAAAGAGGAGAGAGAAAGGGGC	619		
QY	625	TTTCTCCACTGCCAAATATTCAGATAGAGGGAGAGATTAGAGCGGTTCTCAATTTATTCA	684		
Db	620	AGTTTGTATGTTGCGCCATCCAAACAGAGGAGAGATAAAAGCGTTCTGAATTTATTTC	679		
QY	685	GGGCTCCCTCGTCGCTTTCCCGCGAGAAAGTTATGGATGAGCTGAAACATTTCTCTA	744		
Db	680	GGGCTCCCTCATTCGCTTTCCTGGGAGAAAGTTATGGAAGAGGCTGAAATCTTCTCTA	739		
QY	745	CAAAATATTTAAGAGAAAGCCCTGCAAAAGATTCGGGCATCCAGTATACITTTCACTAGAGA	804		
Db	740	AAATATATTTAAGAAAGCCCTTACAAAATATTGCTGTCTCCAGT---CTTTCACGAGAGA	796		
QY	805	TACGGACGTTCTGGAATATGGTTGGCACACCAATTTGCCACGCTTGGAAAGCAAGGAATT	864		
Db	797	TAGAGTACGTTCTGGAGGATGGTTGGCAACAAATATGCCAAGATTTGGAAACAAGGAACT	856		
QY	865	ACATGGACGCTTTTGGACAGCACACACTAAAAATAAG-----AACGCCCGCAGAGAAAC	915		
Db	857	ACATCGATGATTTGGGAGAGAAACGATCGTGATGAGACGTTTATATATGAACATGGAGAAAC	916		
QY	916	TTTTAGAACTTGCAAAATTTGGAATTTCAATATATTTCACTCCTTACAAGAGAGAGAGTTAA	975		
Db	917	TTTTAGAAATTTGCAAAATTTGGAGTTTCAATATATTTTCACTCCTTACAACAGAGAGAGCTAA	976		
QY	976	AACATGTTTCCCGATGTTGGAAAGACTCGGGTTCTCTCTGAGATGACCTTCTGTGACATC	1035		
Db	977	AAGACCTCTCCAGATGTTGGAAAGATTCGGGTTTCTCTCACCTGACATTTTCTCGGCATC	1036		
QY	1036	GTCACGTGGAATACTACGCTTTGGCTTTCCTGCAATTCGGTTCGAGCCTCAACATTTCTGGAT	1095		
Db	1037	GTCAATGTGGAATTTCTACGCTCTGGCATCTTGCAATGAAACTGATCGCAAAACATTCGGAT	1096		
QY	1096	TCAGACTCGGCTTTACCAAGATGTCTCATCTTATCACGGTTCCTTGACGACATGTACGACG	1155		
Db	1097	TCAGACTCGGCTTTGCCAAAATGTGTCATCTTATCACGGTTTTGGACGATATATACGACA	1156		
QY	1156	TCTTCGGCACAGTAGACGAGCTGGAATCTTTCACAGCGACAATTAAGAGATGGGATCCGT	1215		
Db	1157	CCTTTGGAACAATGGAGGAGCTGGAACCTTCTCACTGCAGCATTTAAGAGATGGGATCCGT	1216		
QY	1216	CCGCGATGGAATGCCCTTCCAGAAATATATGAAAGGAGTGTACATGATGGTTTATCACACCG	1275		
Db	1217	CTGCCACAGATTTGCTTCCAGAGTATATGAAAGGGTTGTACATGGTGGTTTACGAAACCG	1276		
QY	1276	TAAATGAAATGGCTCGAGTGGCAGAGAAAGGCTCAAGGCCGAGACACGCTCAACTATGCAA	1335		
Db	1277	TAAATGAAATTTGCTCGAGAGGCAGACAAAGTCTCAAGGCCGAGAGACGCTCAACGATGCTC	1336		
QY	1336	GACAGGCTTGGAGGCGTGTGTTTGTTCGTPATATGCAGGAAGCAAAGTGGATCGCCACTG	1395		
Db	1337	GACGAGCTTGGAGGCCCTATCTTGTATTCGTATATGAAAGAGCTGAGTGGATCTCCAGTG	1396		
QY	1396	GTTATCTGCCACGTTTGGAGAGTACTTTCGAGAAACGGGAAAGTTAGCTCTGCTCATCGCC	1455		
Db	1397	GTTATCTGCCAACGTTTGGAGAGTACATGGAGACCAGCAAGTTAGTTTGGTTATCGCA	1456		
QY	1456	CATGGCAGCTGCAACCCATCTTGACGCTTGGACATCCCCTTTCCCTGATCACATCCTCAAGG	1515		
Db	1457	TATTCGCATTTGCAACCCCATCCTCACTATGGATGTTCCCTTACTCACACATCCTGCAGG	1516		
QY	1516	AAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGTATCATCCTTCGATTAAAGAGTG	1575		
Db	1517	AAATAGACTTTCCATTGAGGTTTAAATGACTTAATATGTTCCATCCTTCGACTTAAAAATG	1576		
QY	1576	ATACACGCTGTACAAAGGCAGACAGGCCCGCTGGAGAAAGCTTTCGTCTATATCATGTT	1635		
Db	1577	ACACTCGCTGTACAAAGCGGACAGGGCCCGTGGAGAAAGCTTTCGTCTATATCGTGT	1636		
QY	1636	ATATGAAAGACAATCCTGGATTAAACGGAGAAGAGATGCTCTGAATCATATCAACTTCATGA	1695		
Db	1637	ATATGAAAGAGATCCTGGATCAACAGAGGAGAGATGCTATCAATCATATCAACGCTATGG	1696		
QY	1696	TCAGGGACGCAATCAGAGAAATTAATTTGGAGCTTCTAAAGCCAGACACAGTGTTCCTCA	1755		
Db	1697	TCAATACCTTAATCAAAGAAAGTGAATTTGGAGCTTCTCCGACAGGACGGCAGCTCATA	1756		
QY	1756	TCACTTCCAAGAAACACGCATTTGACATAACGAGAGTTTGGCATCACGGTTACAGATACC	1815		
Db	1757	TTGCTTGCAAGAAACACGCTTTTGACATCTCTAAAGGTTCCCTTCACGGCTACAATACC	1816		
QY	1816	GAGATGGCTACAGCTTTGCCAACGTTTGAACAAAGAGTTTGGTGTAGAAACCGTCATTG	1875		
Db	1817	GAGATGGGTTTCAGCGTTGCCAACCAAGGAAACCAAGAATTTGGGTGAGGAGAACAGTCCCTG	1876		
QY	1876	AACCTGTGCCCTTTG 1889			
Db	1877	AGTCTGTGCCCTTTG 1890			
RESULT 9					
US-10-025-145A-66					
; Sequence 66, Application US/10025145A					
; Publication No. US20030175861A1					
; GENERAL INFORMATION:					
; APPLICANT: Croteau, Rodney B.					
; APPLICANT: Bohlmann, Joerg					
; APPLICANT: Steele, Christopher L.					
; APPLICANT: Phillips, Michael A.					
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)					
; FILE REFERENCE: WSUR118414					
; CURRENT APPLICATION NUMBER: US/10/025,145A					
; CURRENT FILING DATE: 2002-06-28					



; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1923)
; OTHER INFORMATION:
US-10-025-145A-66

Query Match 53.3%; Score 1072.4; DB 15; Length 2186; Best Local Similarity 76.4%; Pred. No. 8.2e-307; Matches 1428; Conservative 0; Mismatches 391; Indels 51; Gaps 7;					
QY	83	TTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCTTGGAAATCTGCAGGCC	142		
Db	90	TACTCATCATGAGCTCAAGCCTCTGCGCAGAACCATCCCAACTCTTGGAAATGTGTAGGCG	149		
QY	143	GGGAAATCCGTCGCGCATTCATATAAACATGTGTTTGACAAGCGTCGCACTCTACTGATTC	202		
Db	150	AGGGAAATCTTTACACCTTCTGTGAGCATGAGTTGACCACCGCTGTATCTGATGATGG	209		
QY	203	TGTACAGAGACGCGTGGGCAACTATCATTTCCAACTGTGGGACGATGATTTTCATACAGTC	262		
Db	210	TCTACAAAGACGATAGGTGACTATCATTTCCAACTCTCTGGACGACGATTTTCATACAGTC	269		
QY	263	TCTGATCTCAACGCCTTATGGAGCACCTGATTACCGGGAACGTGCTGACAGACTTATTGG	322		
Db	270	TC---TATCAACGCCTTATGGGAGCCTTCTTACCGAGAACGTGCTGAGAAACTGATTGG	326		
QY	323	GGAAAGTAAAGGATATAATGTTTCAATTTCAAGTCGCTGGAAGATGGAG-----	369		
Db	327	GGAAGTGAAGGA---GATGTTTCAATTTCAATGCCATCGGAAGATGGAGATCAATGAGTCC	383		
QY	370	--GCAATGATCTCCTTCAACGACTTTTGTGCTGTCGATGACGTTTGAACGTTTGGGAATCGA	427		
Db	384	CCTCAATGATCTTATTGAACGACTTTGGATGGTCGATAGCGTTTGAACGTTTGGGGATTGA	443		
QY	428	CAGGCATTTCAAAAAAGAGATATAAAACGGCACTCGATTATGTTAACAGTTATTGGAACGA	487		
Db	444	TAGACATTTCAAAAAAGAGATATAAATCAGCCCTTGATTATGTTTACAGTTATTGGAACGA	503		
QY	488	AAAAGGCATTGGATGTGGGAGGAGAGTGTGTGACTGACCTCAACTCAACCGCCTTGGG	547		
Db	504	AAAAGGTATTGGATGCGGTAGAGATAGTGTGTTTCTGATGTCAACTCGACTGCTCGGG	563		
QY	548	GCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGTTTGAACGTTTITAA	607		
Db	564	GTTTCGAACTCTTCGCCTACACGGATACAGTGTCTCTTCAGAGGTTTGAAGTATTTC	623		
QY	608	AGACAAAAATGGGCAATTTTCTCCACTGCCAATATTTCAGATAGAGGGAGAGATTAGAGG	667		
Db	624	AGACCAAAATGGGCAGTTTGCATTTCTCTCC--TAGTACAAAAGAGAGACATCAGAAC	680		
QY	668	CGTTCTCAATTTATTACAGGGCCTCCCTCGTCGCTTTTCCGGCGAGAAAGTTATGGATGA	727		
Db	681	CGTTCTGAATTTATATCGGGCTTCTTTTCATTCGCTTTCTCTGGGAGAAAAGTTATGGAAGA	740		
QY	728	AGCTGAAACATTTCTTACAAAATATTTAAGAGAAAGCCCTGCAAAAGATTCGGCATCCAG	787		
Db	741	GGCTGAAATTTTCTCTTCAAGATATTTGAAGAAAGCCGTGCAAAAGATTCGGTCTCCAG	800		
QY	788	TATACTTTCACTAGAGATACGGGACGTTCTGGAATATGTTTGGCACACCAATTTGCCACG	847		
Db	801	T---CTTTTCAAGAAATAGACTACACTTTGGAATATGTTTGGCACACAAATATGCCAAG	857		

QY	848	CTTGGAAAGCAAGGAATTACATGGACGTCCTTTTGGACAGCACACTA-----AA	893
Db	858	ATTGGAAACAAGGAATTACTTAGATGTATTTTGGACATCTTACCAGTCCATGGCTCAAGAA	917
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QY	894	AATAAGAACGC-----CGCCGAGAAACTTTTGTAGAACTTGC AAAAATTGGAATTCAA	943
Db	918	GAAAAGGACGCAATATCTTGGACAGCGAAAAGCTTTTAGAACTCG AAAAATTGGAGTTCAA	977
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QY	944	TATATTTCACTCTTACAAGAGAGAGAGTTTAAACATGTTTCCCGATGGTGGAAAGACTC	1003
Db	978	CATCTTTCACTCCCTTCAAACAGAGGAGTTTACAGTATCTCTCCAGATGGTGGATACATT	1037
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QY	1004	GGGTTCTCCTGAGATGACCTTCTGTTCGACATCGTCACGTGGAATACTACGCTTTGGCTTC	1063
Db	1038	GGGTTTGCCTGAACTGACCTTTGGTCGGCATCGTCACGTGGAATACTACACCTGAGCTC	1097
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QY	1064	CTGCATTGCGTTCGAGCCCTCAACATTTCTGGATTCAGACTCGGCTTTACCAAGATGTCTCA	1123
Db	1098	TTGCATTTGCGACTGAGCCCAACATTTCTGCATTCAGATTTGGGCTTTGCCAAAACGTGTCA	1157
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QY	1124	TCTTATCACGGTTCCTTGACGACATGTACGACGTCCTTCGGCACAGTAGACGAGCTGGAAC	1183
Db	1158	TCTTATCACGGTTCCTTGACGATATCTACGACACTTCGGAACGATGGATGAAATCGAAC	1217
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QY	1184	CTTCACAGCGCAATTAAGAGATGGATCCGTCGCGCATGGAATGCCCTTCAGAAATATAT	1243
Db	1218	CTTCAAACGAGGCAATTAGGAGATGGAATCCGTCGGAGAAAAGAACGCCCTCCAGAAATAT	1277
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QY	1244	GAAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA	1303
Db	1278	GAAAGAAATCTACATGGCACTCTACGAAGCCTTAACTGACATGGCGCGAGAGCGACAGAA	1337
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QY	1304	GGCTCAAGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGTTGATTC	1363
Db	1338	GACACAAGGCCGAGACACGCTCAATTATGCTAGAAAGGCTTGGGAAGTTTATCTTGATTC	1397
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QY	1364	GTATATGCAGGAAGCAAAAGTGGATCGCCACTGCTGTTATCTGCCCCACGTTTGAGGAGTACT	1423
Db	1398	GTATACACAAGAAGCAAAAGTGGATCGCCAGCGGTTATCTGCCAACTTTCGAGGAGTACT	1457
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QY	1424	GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATCTTGACGTT	1483
Db	1458	AGAGAACGGCAAGGTTAGCTCTGGTCACTGTCAGCGGCAATTGACACCCCTCTGTACATT	1517
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QY	1484	GGACATCCCTTTCCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA	1543
Db	1518	GGACGTACCGCTTCCTGATGACGCTTTGAAAGGGAATAGATTTTCCATCGAGATTTAATGA	1577
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QY	1544	CTTGATATGTATCATCTTCGATTAAAGAGTGATACACGGTGCTACAGGCAGACAGGCG	1603
Db	1578	TTTGGCATCTCTCTTCTTAGACTAAGAGGTGACACACGATGCTACAAGGCAGACAGGGA	1637
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QY	1604	CCGTGGAGAAGAAGCTTCGTCTATATCATGTATTATGAAAGACAAATCCTGGATTAAACGA	1663
Db	1638	CCGAGGAGAAGAAGCGTCAAGCATATCGTGTACATGAAAGACAATCCCGGATTAAACAGA	1697
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QY	1664	AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGAGAAATTAATTG	1723
Db	1698	GGAAGATGCTCTCAATCATATCAATGCCATGATCAACGCACATATCAAAGAATTAATTG	1757
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QY	1724	GGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCACTTCCCATCACTTCCAGAAAACACGC	1783
Db	1758	GGAACCTTCTCAAACCCGATAGCAATATTCCAATGACTGCACGGAACACATGCTTATGAG	1817
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QY	1784	AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTGC CAACGTTTGA	1843
Db	1818	AACCAGAGCTTTCACCAACTTTACAAAATATAGAGATGGCTTCAGCGTTGCCACTCAAGA	1877
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QY	1844	AACAAAGAGTTTGGTATGAGAACCGTCAATGAACTGTGCTGTGCTTTGTAAACAACACTTCA	1903
Db	1878	AACGAAAAGTTTGGTGAGGAGAACGCTCCTTGAACCAAGTGCCTCTTTAACAAATTTAAACC	1937

QY 1904 ATCTACAATA 1913  
Db 1938 TTCTATAATA 1947

RESULT 10

US-09-887-586A-29  
; Sequence 29, Application US/09887586A  
; Patent No. US20020094556A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094556A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/887,586A  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)...(1949)  
; OTHER INFORMATION: myrcene synthase  
US-09-887-586A-29

Query Match 53.2%; Score 1071.6; DB 9; Length 2196;  
Best Local Similarity 75.0%; Pred. No. 1.4e-306;  
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGGTCGTGCCTCAGTTCTTCTCATGAGATTAAAGGTCTCCGTAGAACAAATCCCAACTCT 127  
Db 116 CAAGTCGTTGATCAGTTCAATTCAATGACATAAAGCCTCCCTATAGAACAAATCCCAATCT 175  
QY 128 TGAATCTGCAGGCCGGGAAATCCGTGCGCAATCCATAAACATGTGTTTGACAAGCGT 187  
Db 176 TGAATGCGTAGCGGAGGAAATCTGTCAAGCCTTCCATGAGCATCAGTTTGGCCACCGC 235  
QY 188 CGCATCTACTGATCTGTACAGAGACGCGTGGGCAACTATCATTTCCAACTGTGGGACGA 247  
Db 236 TGCACCTGATGATGGTGTACAAAGACGCATAGGTGACTACCATTTCCAATATCTGGGACGA 295  
QY 248 TGATTTTCATACAGTCTCTGATCTCAACGCCTTATGGAGCACCTGATTACCGGGAACGTGC 307  
Db 296 TGATTTTCATACAGTCTC---TATCAACGCCTTATGGGGAACCCCTCTTACCAGGAACGTGC 352  
QY 308 TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCATTTCAAGTCCGTGCGTGAAGATGG 367  
Db 353 TGAGAGATTAATTGTGGAGGTAAAGAGATA---TTCAATTCAATGTACCTGGATGATGG 409  
QY 368 AGG-----CAATGATCTCCTTCAACGACTTTTGTGTCGATGACGTTGA 412  
Db 410 AAGATTAATGAGTTCCTTTAATGATCTCATGCAACGCCTTGGATAGTCGATAGCGTTGA 469  
QY 413 ACGTTTGGGAATCGACAGGCATTTCAAAAAGAGATAAAAACGGCACTCGATTATGTTAA 472  
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QY 473 CAGTTATTGGAACGAAAAGGCATTTGGATGTGGGAGGAGAGTGTGTTGACTGACCTCAA 532  
Db 530 CCGTTACTGGGAGGAAAACCGGCATTTGGATGTGGGAGAGACAGTATTGTTACTGATCTCAA 589  
QY 533 CTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT 592

Db 590 CTCAACTCGCTGGGGTTTCGAACCTTCGATTACACGGGTACACTGTATCTCCAGAGGT 649  
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Db 650 TTTAAAAGCTTTTCAAGATCAAAATGGACAGTTTGTATGCTCCCCC---GGTCAGACAGA 706  
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Db 707 GGGTGAGATCAGAAAGCGTTCTTAACTTATATCGGGCTTCCCTCATTCGCTTCCCTGGTGA 766  
QY 713 GAAAGTTATGGATGAAGCTGAAACATTTCTCTACAAAATATTAAAGAGAAGCCCTGCAAAA 772  
Db 767 GAAAGTTATGGAAGAAGCTGAAATCTTCTCCACAAGATATTGAAAGAAGCTCTACAAAA 826  
QY 773 GATTCCGGCATCCAGTATACCTTCTACTAGAGATACGGGACGTTCTTGGAAATATGGTTGGCA 832  
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Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAAGACACCAG 943  
QY 892 -----AAAATAAGAACGCCGCCGAGRAACTTTTAGAACTTTGCAAAATTTGGAATTCAA 943  
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QY 1304 GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTGTTGATTC 1363  
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QY 1424 GGAGAACGGGAAAGTTAGCTCTGTCTCATCGCCCATGCGCACTGCAACCCATTTCTGACGTT 1483  
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QY 1484 GGACATCCCTTTTCTTGATCACATCTTCAAGGAAGTGTGACTTCCCATCGAAGCTCAATGA 1543  
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QY 1544 CTTGATATGTATCATCTTCTCGATTAAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGC 1603  
Db 1604 TTTGGCATCGTCTTCTTCCGCTACGAGGTGACACAGCTGTCTACAAGGCCGATAGGA 1663  
QY 1604 CCGTGGAGAAAGAGCTTCGTCTATATCATGTTTATGAAAGACAATCTCTGGATTAAACGA 1663

Db 1664 TCGTGGTGAAGAAGCTTCGTGTATATCATGTTATATGAAGAACAATCCTGGATCAACCGA 1723  
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Db 1724 AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATAATCAAAGAAATTAAATTG 1783  
QY 1724 GGAGCTTCTAAAGCAGACAACAGTGTTCCTCATCTCCATCACTTCCAAGAAACACGCAATTGACAT 1783  
Db 1784 GGAACCTTCTAAGATCCAACGACAATATTCCAATGCTGCCAAGAAACATGCTTTTGACAT 1843  
QY 1784 AAGCAGAGTTTGGCAFCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843  
Db 1844 AACAAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGGCCAAACAAGGA 1903  
QY 1844 AACAAAGAGTTTGGTGATGAGAACCGTCACTTGAACCTGTGCCTTTGTAAACAACACTTCAA 1903  
Db 1904 AACAAAAAATTGGTTATGGAACAACACTCCTTGAATCTATGCTTTTAACTATAACCATA 1963  
QY 1904 ATCTACAATATTAACTGAGGATGCCCTATGGGTGTATATAGGGCACA 1950  
Db 1964 TCCATAATAATAAGCTCATAATGCTAAATTATTGSCCTTATGACATA 2010

RESULT 11  
US-09-903-012-29  
; Sequence 29, Application US/09903012  
; Patent No. US20020094557A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094557A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/903,012  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,993  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)...(1949)  
; OTHER INFORMATION: myrcene synthase  
US-09-903-012-29

Query Match 53.2%; Score 1071.6; DB 9; Length 2196;  
Best Local Similarity 75.0%; Pred. No. 1.4e-306;  
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;  
QY 68 CAGGTCGTGCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCCCAACTCT 127  
Db 116 CAAGTCGTTGATCAGTTCAATTCAATGAACATAAGCCTCCCTATAGAACAAATCCCAATCT 175  
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Db 176 TGAATGCGTAGCGGAGGGAATCTGTACGCTTCCATGAGCATCAGTTTGGCCACCGC 235  
QY 188 CGCATCTACTCAATTCTGTACAGAGACGCGTGGGCAACTATCATTCCAACCTGTGGGACGA 247  
Db 236 TGCACCTGATGTTGTACAAAGACGCATAGGTGACTACCATTCCTCAATATCTGGGACGA 295  
QY 248 TGATTTTCATACAGTCTCTGATCTCAACGCTTATGGAGCACCTGATTACCGGGAACGTGC 307

Db 296 TGATTTTCATACAGTCTC---TATCAACGCCTTATGGGAAACCCCTCTTACCAGGAACGTGC 352  
QY 308 TGACAGACTTATTGGGGAAGTAAAGGATATAATGTTCAAATTTCAAGTCGCTGGAAGATGG 367  
Db 353 TGAGAGATTAAATTGTGAGGTTAAAGAAGATA---TTCAAATTCAATGTACTCTGGATGATGG 409  
QY 368 AGG-----CAATGATCTCCTTCAACGACTTTTGTCTGGTCGATGACGTTGA 412  
Db 410 AAGATTAAATGAGTTCCCTTTAAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGA 469  
QY 413 ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTTATGTTAA 472  
Db 470 ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATAAATCAGCTCTGGATTATGTTT 529  
QY 473 CAGTTATTGGAACGAAAAAGGCATTTGGATGTGGAGGGAGAGTGTGTGTGACTGACCTCAA 532  
Db 530 CCGTTACTGGGAGGAAAAACGGCATTTGGATGTGGAGAGACAGTATTGTTTACTGATCTCAA 589  
QY 533 CTCAACCGCCTTGGSGCTTCGAACTCTCCGACTACACGGGATACACTGTGTCTTCAGATGT 592  
Db 590 CTCAACTGCGTTGGGCTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT 649  
QY 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATTCAGATAGA 652  
Db 650 TTTAAAAGCTTTTCAAGATCAAAATGGACAGTTGTATGCTCCCC---GGTCAGACAGA 706  
QY 653 GGGAGAGATTAGAGCGCTTCTCAATTTATTAGGGGCTCCCTCGTCGCTTCCCGCGCA 712  
Db 707 GGGTGAGATCAGAAGCGTTCTTAACTTATATCGGGCTTCCCTCATTTGCCCTTCCCTGGTGA 766  
QY 713 GAAAGTTATGGATGAAGCTGAAACATTCTCTACAAAAATATTAAAGAGAAAGCCCTGCAAAA 772  
Db 767 GAAAGTTATGGAAGAAAGCTGAAATCTTCTCCACAAGATATTGAAAGAAAGCTCTACAAA 826  
QY 773 GATTCCGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTTGGAAATATGGTTGGCA 832  
Db 827 GATTCCAGTCTCCGCT---CTTTCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCA 883  
QY 833 CACCAATTTGCCACGCTTGGAAAGCAAGGAATTACATGGACGCTCTTTGGACAGCACACTA- 891  
Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAAGACACCAG 943  
QY 892 -----AAAAATAAGAACGCCGCCAGAGAGTTTAAACCATGTTTCCCGATGGTGGAAAGACTC 943  
Db 944 TGCATGGCTCAATAAAAAATGCTGGGAAGAAGCTTTTAGAACTTGC AAAATTGGAGTTTCAA 1003  
QY 944 TATATTTCACTCTTACAAGAGAGAGAGATTAAAAACATGTTTCCCGATGGTGGAAAGACTC 1003  
Db 1004 TATATTTAACTCCTTACAACAAAAAGGAATTACAATATCTTTTGAGATGGTGGAAAGAGTC 1063  
QY 1004 GGGTTCTCCTGAGATGACCTTCTGTCCGACATCGTCACGTGGAATACTACGCTTTGGCTTC 1063  
Db 1064 GGAATTTGCCCTAAAATTGACATTTGCTCGGCATCGTCATGTGGAATTTCTACACTTTGGCCTC 1123  
QY 1064 CTGCATTGCGTTCGAGCCTCAACATTTCTGGATTCTAGACTCGGCTTTTACCAAGATGTCTCA 1123  
Db 1124 TTGTATTGCCATTGACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCA 1183  
QY 1124 TCTTAICACGGTTCTTGACGACATGTACGACGTTCTTCGGCACAGTAGACGAGCTGGAAC 1183  
Db 1184 TCTTGTACAGTTTGGACGATATTATTACGACACTTTTGGAAACGATTGACGAGCTTGAAC 1243  
QY 1184 CTTACAGCGGACAAATTAAGAGATGGGATCCGTCCGGATGGAATGTCCTTCCAGAATATAT 1243  
Db 1244 CTTACATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGAATATAT 1303  
QY 1244 GAAAGGAGTGATCATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA 1303  
Db 1304 GAAATGTGTACATGGTCGTGTTTGAACACTGTAATGAACCTGACACGAGAGCGGAGAA 1363  
QY 1304 GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGTTTGATTC 1363



Db	1364	GACTCAAGGAGAGAAACACTCTCAACTATGTTTCGAAAGGCTTGGAGGGCTTATTTTGATT	1423
QY	1364	GTATATGCGAAGCAAAAGTGGATCGCACTGGTTATCTGCCACGTTTGAGGAGTACTT	1423
Db	1424	ATATATGGAAGAGCAAAATGGATCTCTAAATGGTTATCTGCCAATGTTTGAAGAGTACCA	1483
QY	1424	GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATCGGCACTGCAACCCATCTGACGTT	1483
Db	1484	TGAGAAATGGAAAGTGAGCTCTGCATATCGGTAGCAACATTGCAACCCATCCTCACTTT	1543
QY	1484	GGACATCCCTTTTCCTGATCATCATCTCAAGAAAGTTGACTTCCCATCGAAAGCTCAATGA	1543
Db	1544	GAATGCATGGCTTCCTGATTACATCTTGAAGGGAATTGATTTTCCATCCAGGTTCAATGA	1603
QY	1544	CTTGATATGATCATCTCTTCGATTAAAGAGGTGATACACGGTGCTACAGGCAGACAGGGC	1603
Db	1604	TTTGGCATCGTCTTCCTTCGGCTACGAGGTGACACACGCTGCTACAAAGCCGATAGGGA	1663
QY	1604	CCGTGGAGAAAGCTTCGTCTATATCATGATCAGGGACGCAATCGGTAAACCGGA	1663
Db	1664	TCGTGGTGAAGAGCTTCGTGTATATCATGTTATATGAAAGACAATCCCTGGATCAACCGA	1723
QY	1664	AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGAGAATTAAATTG	1723
Db	1724	AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATAATCAAGAATTAATG	1783
QY	1724	GGAGCTTCTAAAGCCAGACAAACAGTGTTCCTCATCACTTCCAAGAAACACGCAATTTGACAT	1783
Db	1784	GGAACCTTCTAAGATCCAACGACATATTTCCAAATGCTGGCCCAAGAAACATGCTTTTGACAT	1843
QY	1784	AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA	1843
Db	1844	AACAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAGGA	1903
QY	1844	AACAAGAGTTTGGTGTATGAGAACCGTCAATTGAACCTGTGCCTTTGTATAACACACTTCAA	1903
Db	1904	AACAAAAAAATTGGTTATGGAACACTCCCTTGAATCTATGCTTTTAACTATAACCAT	1963
QY	1904	ATCTACAATATTAAGTGGAGATGCCCTATGGGTGTATATAGGGCACA	1950
Db	1964	TCCATAATAATAAGCTCATAATGCTAAATTTATGGCCTTATGACATA	2010

RESULT 12

US-09-900-797-29

Sequence 29, Application US/09900797

Publication No. US20030087406A1

GENERAL INFORMATION:

APPLICANT: Chappell, Joseph

APPLICANT: No. US20030087406A11, Joseph P.

APPLICANT: Starks, Courtney M.

APPLICANT: Manna, Kathleen R.

TITLE OF INVENTION: SYNTHASES

FILE REFERENCE: 07678-025001

CURRENT APPLICATION NUMBER: US/09/900,797

CURRENT FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: US/09/398,395

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: 60/130,628

PRIOR FILING DATE: 1999-04-22

PRIOR APPLICATION NUMBER: 60/150,262

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 29

LENGTH: 2196

TYPE: DNA

ORGANISM: Abies grandis

FEATURE:

NAME/KEY: CDS

LOCATION: (69)...(1949)

OTHER INFORMATION: myrcene synthase

US-09-900-797-29

Query Match		53.2%;	Score 1071.6;	DB 10;	Length 2196;
Best Local Similarity		75.0%;	Pred. No. 1.4e-306;		
Matches 1430;		Conservative	0;	Mismatches 441;	Indels 36; Gaps 6;
68	CAGGTCGTGCCTCAGTTCCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT	127			
116	CAAGTCGTTGATCAGTTCAATTTCATGAACATAAAGCCTCCCTATAGAACAAATCCCAATCT	175			
128	TGGAATCTGCAGGCCGGGAAATCCGTCGCGCATTCATATAACATGTTTGTACAAGCGT	187			
176	TGGAATGCGTAGCGGAGGGAATCTGTACGCCCTTCCATGAGCATCAGTTTGGCCACCGC	235			
188	CGCATCTACTGATTTCTGTACAGAGACGCGTGGGCAACTATCATTTCCAACCTGTGGGACGA	247			
236	TGCACCTGATGATGGTGTACAAAGACGCATAGGTGACTACCATTCCAATATCTGGGACGA	295			
248	TGATTTCTATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTAACGGGAACGTGC	307			
296	TGATTTCTATACAGTCTC---TATCAACGCCCTTATGGGAACCCCTCTTACCAGGAACGTGC	352			
308	TGACAGACTTATTGGGGAAGTAAAGGATATAAATGTTTCAATTTCAAGTCGCTGGAAGATGG	367			
353	TGAGAGATTAAATTGTGGAGGTAAGAAGATA--TTCAATTCAATGTACCTGGATGATGG	409			
368	AGG-----CAATGATCTCCTTCAACGACTTTTGTGTCGATGACGTTGA	412			
410	AAGATTAATGAGTTCCTTTAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGA	469			
413	ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACCTCGATTATGTTAA	472			
470	ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTT	529			
473	CAGTTATTGGAAACGAAAAAGGCATTGGATGTGGGAGGGAGAGTGTGTGACTGACCTCAA	532			
530	CCGTTACTGGAGGAAAAACGGCATTGGATGTGGGAGAGACAGTATTGTTACTGATCTCAA	589			
533	CTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATACACTGTGTCTTCCAGATGT	592			
590	CTCAACTGCGTTGGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT	649			
593	TTTGAAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATTCAGATAGA	652			
650	TTTAAAGCTTTTCAAGATCAAAATGGACAGTTTGTATGCTCCCC--GGTCAGACAGA	706			
653	GGGAGAGATTAGAGCGCTTCTCAATTTATTTCAGGGCCTCCCTCGTCGCCCTTCCCGCGCA	712			
707	GGGTGAGATCAGAAGCGTTCTTAACCTTATATCGGGCTTCCCTCATTTGCCCTTCCCTGGTGA	766			
713	GAAAGTTATGGATGAAGCTGAAACATTTCTTACAAAAATATTTAAGAGAGAGCCCTGCAAAA	772			
767	GAAAGTTATGGAAGAGCTGAAATCTTCTCCACAAGATATTTGAAAGAGAGCTCTACAAAA	826			
773	GATTCGGGCATCCAGTATACCTTTCATAGAGATACGGGACGTTCTGGAAATATGTTGGCA	832			
827	GATTCAGTCTCCGCT---CTTTCAAGAGATAAAGTTTGTATTGGAATATGGCTGGCA	883			
833	CACCAATTTGCCACGCTTGGAAAGCAAGGAATTACATGGACGCTCTTTGGACAGCACACTA-	891			
884	CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAG	943			
892	-----AAAATAAGAACGCCGCCGAGAAACTTTTAGAACTTTGCAAAATTTGGAATCAA	943			
944	TGCATGGCTCAATAAAAAATGCTGGGAAGAGCTTTTAGAACTTTGCAAAATTTGGAGTTCAA	1003			
944	TATATTTCACTCTTACAAAGAGAGAGATTAAAAACATGTTTCCCGATGGTGGAAAGACTC	1003			
1004	TATATTTAACTCTTACAAACAAAGGAATTACAATATCTTTTGGATGTTGGAAAGAGTC	1063			
1004	GGGTTCTCCTGAGATGACCTTCTGTGACATCGTCACGTGGGAATACTACGCTTTGGCTTC	1063			
1064	GGATTTGCCTAAATTGACATTTGCTCGGCATCGTCATGTGGAATTTCTACACTTTGGCCTC	1123			



QY	1064	CTGCATTGCGTTTCGAGCCTCAACATCTCTGGATTTCAGACTCGGCTTTACCAAGATGTCCTCA	1124
Db	1124	TTGTATTGCCATTGACCCAAAAACATCTGTCAATTCAGACTAGGCTTCGCCAAAATGTCCTCA	1183
QY	1124	TCTTATCACGGTCTTTGACGACATGTACGACGCTCTTCGSCACAGTAGACGAGCTGGAAT	1183
Db	1184	TCTTGTACAGTTTTGGACGATATTACGACACTTTTGAACGATTTGACGAGCTTGAAT	1243
QY	1184	CTTCACAGCGACAATTAAGAGATGGATCCGTCGCGGATGGAATGCCCTTCAGAAATATAT	1243
Db	1244	CTTCACATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCAGAAATATAT	1303
QY	1244	GAAGGAGTGTACATGATGGTTTTATCACACCGCTAAATGAAATGGCTCGAGTGGCAGAGAA	1303
Db	1304	GAATGTGTGTACATGGTCGTGTTTGAACCTGTAATGAACTGACACGAGAGCGGAGAA	1363
QY	1304	GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTTTGATTC	1363
Db	1364	GACTCAAGGGAGAAACACTCTCAACTATGTTTCGAAAGGCTTGGGAGGCTTATTTGATTC	1423
QY	1364	GTATATGCAGGAAGCAAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCGACGTT	1423
Db	1424	ATATATGGAAGAAGCAAAATGGATCTCTAATGGTTATCTGCCAATGTTTGAAGAGTACCA	1483
QY	1424	GGAGAACGGGAAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCGACGTT	1483
Db	1484	TGAGAAATGGGAAAAGTGAGCTCTGCATATCGCGTAGCAACATTTGCAACCCATCTCACTTT	1543
QY	1484	GGACATCCCCCTTTCCTGATCACATCCTCAAGGAGTTGACTTCCCATCGAAGCTCAATGA	1543
Db	1544	GAATGCATGGCTTCTGTATTACATCTTGAAGGGAATGATTTCCATCCAGGTTCAATGA	1603
QY	1544	CTTGATATGTATCATCCTTCGATTAGAGGTTGATACACGGTGCTACAAGGCAGACAGGC	1603
Db	1604	TTTGGCATCGTCCCTTCTTGGCTACGAGGTGACACAGCTGCTACAAGGCCGATAGGGA	1663
QY	1604	CCGTGGAGAAAGCTTCGTCTATATCATGTTATATGAAAGACAAATCCTGGATTAAATG	1663
Db	1664	TCGTGGTGAAGAAAGCTTCGTGTATATCATGTTATATGAAAGACAAATCCTGGATCAACCGA	1723
QY	1664	AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAAATTAATG	1723
Db	1724	AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATAATCAAAGAAATTAATG	1783
QY	1724	GGAGCTCTAAAGCCAGACAACAGTGTTCCTCATCACTTCCAAGAAACACGCATTTGACAT	1783
Db	1784	GGAACCTCTAAGATCCAACGACAAATATCCAATGCTGGCCAAGAAACATGCTTTTGACAT	1843
QY	1784	AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA	1843
Db	1844	AACAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAGGA	1903
QY	1844	AACAAAGAGTTTGGTGATGAGAACCGTCATTGAACTGTGCCTTTTGTAAACAACACTTCAA	1903
Db	1904	AACAAAAAATTTGGTTATGGAAACACTCCCTTGAATCTATGCTTTTTTAACTATAACCATAT	1963
QY	1904	ATCTACAATATTAACTGAGGATGCCCTATGGGTGTATATAGGGCACA	1950
Db	1964	TCCATAATAATAGCTCATAAATGCTAAATTTATGGCCTTATGACATA	2010

## RESULT 13

```

US-09-893-820-29
; Sequence 29, Application US/09893820
; Publication No. US2004005386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US2004005386A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893.820

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QY	773	GATTCGGCATCCAGTATAC	TTTCACTAGAGATACGGGACGTTCTTGGAAATATGGTTGGCA	832
Db	827	GATTCAGTCTCGCT---	CTTCAAGAGATAAAGTTTGTATGGAATATGGCTGGCA	883
QY	833	CACCAATTTGCCACGCTT	TGGAAGCAAGGAATTACATGGACGTC	891
Db	884	CACAAATTTGCCAAGATT	TGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAG	943
QY	892	-----	AAAATAAGAACGCCCGCAGAAACTTTT	943
Db	944	TGCATGGCTCAATAA	AAATGCTGGGAAGAACCTTTAGAACTT	1003
QY	944	TATATTTCACTCTCTTA	CAAGAGAGAGAGATTAAACATGTTTCCCGATGGTGGAAAGACTC	1003
Db	1004	TATATTTAACTCCCTT	ACAAAGGAATTACAAATATCTTTTGAGATGGTGGAAAGAGTC	1063
QY	1004	GGGTTCTCCTGAGATGACCTT	CTGTTCGACATCGTCACGTGGAATACTACGCTTTGGCTTC	1063
Db	1064	GGATTTGCCTAAATTTGACATTT	TGCTCGGCATCGTCATGTGGAATTTACACATTTGGCCTC	1123
QY	1064	CTGCATTTGCGTTTCGAGCCT	CAACATTTCTGGAATTCAGACTCGGCTTTACCAAGATGTCTCA	1123
Db	1124	TTGTATTTGCCATTTGACCCAA	AACATTTCTGCAATTCAGACTAGGCTTCGCCAAATGTGTCA	1183
QY	1124	TCATTACCGGTTCTTGACGACAT	GTACGACGCTTTCGGCACAGTAGACGAGCTGGAAC	1183
Db	1184	TCTTGTACAGTTTTTGGACGATAT	TTTACGACACTTTTGGAACGATTGACGAGCTTGAAC	1243
QY	1184	CTTACAGCGACAAATAAGAGAT	GGGATCCCGTCCCGATGGAATGCCTTCCAGAAATATAT	1243
Db	1244	CTTCACATCTGCAATTAAGAGAT	GGAATTCATCAGAGATAGAACACCTTCCAGAAATATAT	1303
QY	1244	GAAAGGAGTGTACATGATGGTTT	TATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA	1303
Db	1304	GAAATGTGTACATGGT	CGTGTGAAACTGTAAATGAACTGACACGAGAGCGGAGAA	1363
QY	1304	GGCTCAAGGCCGAGACACGCT	CAACTATGCAAGACAGGCTTGGGAGCGGTGTTTGAATTC	1363
Db	1364	GACTCAAGGGAGAAACACTCT	CAACTATGTTTCGAAAGGCTTGGGAGGCTTATTTTGAATTC	1423
QY	1364	GTATATGCAGGAAGCAAGTGGAT	CGCCACTGGTTATCTGCCACAGTTTGAGGAGTACTT	1423
Db	1424	ATATATGGAAGAACCAAAATGGAT	CTCTAATGGTTATCTGCCAATGTTTGAAGAGTACCA	1483
QY	1424	GGAGAACGGGAAAGTTAGCTCT	GTCTCATCGCCCATGCGCACTGCAACCCATTTCTGACGTT	1483
Db	1484	TGAGAAATGGGAAAGTAGCTCT	GCATATCGCGTAGCAACATTTGCAACCCATCTCTACTTT	1543
QY	1484	GGACATCCCCTTTCTGATCACAT	CTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA	1543
Db	1544	GAAATGCATGGCTTCCTGATTACAT	CTTTGAAGGGAATTGATTTTCCATCCAGGTTCAATGA	1603
QY	1544	CTTGATATGTATCATCTCTCGA	TTAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGC	1603
Db	1604	TTTGGCATCGTCTCTCTCGGCT	ACGAGGTGACACACGCTGTCTACAAGGCCGATAGGGA	1663
QY	1604	CCGTGGAGAAGAGCTTCGTCT	TATATCATGTTATATGAAGACAAATCCTGGATTAAACGA	1663
Db	1664	TCGTGGTGAAGAGCTTCGTGT	ATATCATGTTATATGAAGACAAATCCTGGATCAACCGA	1723
QY	1664	AGAAGATGCTCTGAATCATAT	CAACTTCATGATCAGGAGCGCAATCAGAGAATTAATTTG	1723
Db	1724	AGAAGATGCCCTCAATCATAT	CAATCAATGCCATGGTCAATGACATAATCAAGAATTAATTTG	1783
QY	1724	GGAGCTTCTAAAGCCAGACAA	CAGTGTTCCTCCATCACTTCCAAGAAACACGCAATTTGACAT	1783
Db	1784	GGAACTTCTAAGATCCAACG	CAATATTTCCAATGCTGGCCAAAGAAACATGCTTTTGACAT	1843
QY	1784	AAGCAGAGTTTGGCATCAC	GGTTTACAGATACCGAGATGGGTACAGCTTTTGCCAAACGTTGA	1843
Db	1844	AACAAGAGCTCTCCACC	ATCTCTACATATATCGAGATGGCTTTAGTGTGGCCAAACAGGA	1903
QY	1844	AACAAAGAGTTTGGTGAT	GAGAACCGTCATTTGAACCTGTGCTTTTGTAAACAACATTTCAA	1903

Db 1904 AACAAAAAAATGGTTATGGAAACACCTCCTTGAATCTATGCTTTTTTAACTATAACCATA 1963

QY 1904 ATCTACAATATTAACCTAGGATGCCCTATGGTGTATATAGGGCACA 1950

Db 1964 TCCATAATAATAAGCTCATAATGCTAAATTATTGGCCCTTAGACATA 2010

RESULT 14

US-10-041-007-25

; Sequence 25, Application US/10041007

; Publication No. US20020164736A1

; GENERAL INFORMATION:

; APPLICANT: Matsuda, Seiichi P.T.

; APPLICANT: Schepmann, Hala G

; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

; FILE REFERENCE: P02081US1

; CURRENT APPLICATION NUMBER: US/10/041,007

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: US 60/259,881

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 2196

; TYPE: DNA

; ORGANISM: Abies grandis

US-10-041-007-25

Qy

QY 653 GGGAGAGATTAGAGCGTTCTCAATTTATTACAGGGCTCCCTCGTCGCCCTTTCCCGCGGA 712  
Db 707 GGGTGAGATCAGAAAGCGTTCTTAACCTTATATCGGGCTTCCCTCATTCGCTTCCCTGGTGA 766  
QY 713 GAAAGTTATGGATGAAGCTGAAACATTCTCTACAAATATTTAAGAGAAGCCCTGCAAAA 772  
Db 767 GAAAGTTATGGAAGAAGCTGAAATCTTCTCCACAAGATATTTGAAAGAAGCTCTACAAA 826  
QY 773 GATTCCGGCATCCAGTATACTTTTCACTAGAGATACGGGACGTTCTTGGAATATGTTGGCA 832  
Db 827 GATTCCAGTCTCCGCT---CTTTCACAAGAGATAAAAGTTTGTATGGAATATGCTGGCA 883  
QY 833 CACCAATTTGCCACGCTTGGAAGCAAGGAATTACATGGACGTCCTTTGGACAGCACACTA- 891  
Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGRAAGACACCAG 943  
QY 892 -----AAAATAAGAACGCCGCCGAGAAAACITTTTAGAACTTGCAAAATTGGAAATCAA 943  
Db 944 TGCATGGCTCAATAAAAATGCTGGGAAGAAGCTTTTAGAACTTGCAAAATGGAGTTCAA 1003  
QY 944 TATATTTCACTCTTACAAGAGAGAGAGAGTTAAAACATGTTTCCCGATGGTGGAAAAGACTC 1003  
Db 1004 TATATTTAACTCTTACAACAAAAGGAATTACAATATCTTTTGAGATGGTGGAAAAGATC 1063  
QY 1004 GGGTTCTCTGAGATGACCTTCTGTGACATCGTCACGTGGAATACACTACGTTTGGCTTC 1063  
Db 1064 GGATTTGCCTAATTGACATTTGCTCGGCATCGTCATGTGGAATTTCTACACTTTGGCCTC 1123  
QY 1064 CTGCATTCGTTTCGAGCCTCAACATTTCTGATTCAGACTCGGCTTTTACCAAGATGTCCTCA 1123  
Db 1124 TTGTATTGCCAATGACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCA 1183  
QY 1124 TCTTATCACGGTTCTTTGACGACATGTACGACGTCCTTCGGCACAGTAGACGAGCTGGAAC 1183  
Db 1184 TCTTGTACACAGTTTGGACGATATTTACGACACTTTTGAACGATTGACGAGCTTGAAC 1243  
QY 1184 CTTACAGCGCAAAATTAAGAGATGGGATCCGTCGGCGATGGAATGCCCTTCCAGAAATATAT 1243  
Db 1244 CTTACATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGAAATATAT 1303  
QY 1244 GAAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA 1303  
Db 1304 GAAATGTGTATACATGGTCGTGTTTGAACTGTAAATGAACTGACACGAGAGCGGAGAA 1363  
QY 1304 GGCTCAAGCGCAGACACGCTCAACTATGCAAGA CAGGCTTGGGAGGCGTGTTTGATTC 1363  
Db 1364 GACTCAAGGGAGAAAACACTCTCAACTATGTTTCGAAAAGGCTTGGGAGGCTTATTTTGATTC 1423  
QY 1364 GTATATGCAGGAAGCAAAAGTGGATCGCATCGCACTGGTTATCTGCCACGTTTGAGGAGTACTT 1423  
Db 1424 ATATATGGAAGAAGCAAAATGGATCTCTAATGGTTATCTGCCAATGTTTGAAGAGTACCA 1483  
QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATCGCCTGCACTGCAACCCATTCGACGTT 1483  
Db 1484 TGAGAAATGGGAAAGTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCCTCACITT 1543  
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Db 1544 GAATGCATGSGCTTCTGTATTACATCTTGAAGGAATTGATTTTCCATCCAGGTTCAATGA 1603  
QY 1544 CTTGATATGTATCATCCTTCGATTAAGAGGTGATACACGGTGCTTACAAGGCAGACAGGGC 1603  
Db 1604 TTTGGCATCGTCCTTCTTCGGCTACGAGTGACACACGCTGCTACAAGGCCGATAGGGA 1663  
QY 1604 CCGTGAGAGAAGCTTCGCTATATATGTTATATGAAAGACAAATCCTGGATTAACGGA 1663  
Db 1664 TCGTGGTGAAGAAGCTTCGTGTATATCATGTTATATGAAAGACAAATCCTGGATCAACCGA 1723  
QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGACGCAATCAGAGAATTAATTTG 1723  
Db 1724 AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATATCAAGAATTAATTTG 1783  
QY 1724 GGAGCTTCTAAAGCCGACACAACAGTGTTCCTCATCACTTCCAAAGAAACACGCATTTGACAT 1783

RESULT 15

US-10-025-145A-1

; Sequence 1, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Abies Grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)..(1952)  
; OTHER INFORMATION:  
US-10-025-145A-1

Query Match 53.2%; Score 1071.6; DB 15; Length 2196;  
Best Local Similarity 75.0%; Pred. No. 1.4e-306;  
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGGTGTCGCTCAGTTCCTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCCCAACTCT 127  
Db 116 CAAGTCGTGTGATCAGTTCATTCATGAACATAGCCTCCCTATAGAACAAATCCCAATCT 175  
QY 128 TGGAAATCTGCAGGCCGGGAAATCCGTGCGGCATTCCATAAACATGTGTTTGACAAGCGT 187  
Db 176 TGGAAATCGTAGCGGAGGAAATCTGTACAGCCTTCCATGAGCATCAGTTTGGCCACCGC 235  
QY 188 CGCATCTACTGATTCTGTACAGAGACGCGTGGGCAACTATCATTCACACCTGTGGGACGA 247  
Db 236 TGCACCTGATGATGGTGTACAAAGACGCATAGGTGACTACCATTCCAATATCTGGGACGA 295  
QY 248 TGATTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGGAACGTGC 307  
Db 296 TGATTTCATACAGTCTC---TATCAACGCCCTTATGGGGAACCTCTTACCAGGAACGTGC 352  
QY 308 TGACAGACTTATTGGGAAGTAAGGATATAATGTTCATTTCAAGTCGCTGGAAGATGG 367  
Db 353 TGAGAGATTAATTGTGGAGGTAAGAAGATA---TTCAATTCATGTACCTGGATGATGG 409  
QY 368 AGG-----CAATGATCTCCTTCAACGACTTTTGCTGGTCGATGACGTTGA 412



Db 410 AAGATTAATGAGTTCCTTTAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGA 469

QY 413 ACGTTTCGGAATCGACAGGCAATTCAAAAAGAGATAAAAACGGCACTCGATTATGTTAA 472

Db 470 ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTT 529

QY 473 CAGTTATTGGAACGAAAAAGGCATTGGATGTGGAGGGAGAGTGTGTGACTGACCTCAA 532

Db 530 CCGTTACTGGGAGGAAAAACGGCAATTGGATGTGGAGAGACAGTATTGTTACTGATCTCAA 589

QY 533 CTCAACCGCTTGGGGCTTCGAACCTCTCCGACTACACGGATACACTGTGTCTTCAGATGT 592

Db 590 CTCAACTGCGTTGGGGTTTCGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT 649

QY 593 TTTGAACGTTTTAAAGACAAAAAATGGGCAATTTTCTCCACTGCCAATATTTCAGATAGA 652

Db 650 TTTAAAAGCTTTTCAAGATCAAAAATGGACAGTTTGTATGCTCCCC---GGTCAGACAGA 706

QY 653 GGGAGAGATTAGAGCGGTTCTCAATTTATTCAGGGCCTCCCTCGFCGCCCTTCCCGCGA 712

Db 707 GGGTGAGATCAGAAGCGTCTTAACTTATATCGGGCTTCCCTCAATTGCGCTTCCCTGGTGA 766

QY 713 GAAAGTTATGATGAAGCTGAAACATTTCTTACAAAATATTTAAGAGAGACCCCTGC AAA 772

Db 767 GAAAGTTATGGAAGAAGCTGAAATCTTCTCCACAAGATATTTGAAAGAGCTCTACAAA 826

QY 773 GATTCGGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTCGAATATGTTGGCA 832

Db 827 GATTCAGTCTCCGCT---CTTTACAGAGATAAAGTTTGTATGGAATATGGCTGGCA 883

QY 833 CACCAATTTGCCAGCTTGGAGCAAGGAATTACATGGACGTCCTTTGGACAGCACACTA- 891

Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTTGAGAAAGACACCAG 943

QY 892 -----AAAAFAAGAACGCCCGAGAAAATTTTAGAACTTGC AAAATTGGAATTC AA 943

Db 944 TGCATGGCTCAATAAAAAATGCTGGGAAGAGCTTTTAGAACTTGC AAAATTGGAGTTCAA 1003

QY 944 TATATTTCACTCCTTACAAGAGAGAGAGTTTAAAAACATGTTTCCCGATGGTGGAAAGACTC 1003

Db 1004 TATATTTAACTCCTTACAACAAAAGGAATTACAATATCTTTTGAGATGGTGGAAAAGAGTC 1063

QY 1004 GGGTCTCTCGATGACCTTCTGTGACATCGTCACGTGGAATACTACGCTTTGGCTTC 1063

Db 1064 GGATTTGCCCTAATTGACATTTGCTCGGCATCGTCATGTGGAATTCTACACTTTGGCCTC 1123

QY 1064 CTGCATTGCGTTCGAGCCTCAACATTTCTGGATTTCAGACTCGGCTTTTACCAGATGTCTCA 1123

Db 1124 TTGTATTGCCATTGACCCAAAACATTTCTGCATTTCAGACTAGGCTTCGCCAAAATGTGTC A 1183

QY 1124 TCTTATCACGGTTCCTTGACGACATGTACGACGTCCTTCGGCACAGTAGACGAGCTGGAAC T 1183

Db 1184 TCTTGTACAGTTTTTGGACGATATTTACGACACTTTTGGAACGATTGACGAGCTTGAAC T 1243

QY 1184 CTTACAGCGACAAATTAAGAGATGGGATCCGTCGCGATGGAATGCTTCAGAAATATAT 1243

Db 1244 CTTACATCTGCAATTAAAGAGATGGAAATTCATCAGAGATAGAACACTTCCAGAAATATAT 1303

QY 1244 GAAAGGAGTGATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAA 1303

Db 1304 GAAATGTGTACATGCTCGTGTTTTGAAACTGTAAATGAACTGACACGAGAGCGGAGAA 1363

QY 1304 GGCTCAAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTTTTGATTC 1363

Db 1364 GACTCAAGGGAGAAACACTCTCAACTATGTTTGGAAAGGCTTGGGAGGCTTATTTGATTC 1423

QY 1364 GTATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCACGTTTGGAGAGTACTT 1423

Db 1424 ATATATGGAAGAAGCAAAATGGATCTCTAATGGTTATCTGCCAATGTTTGAAGAGTACCA 1483

QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGGCACTGCAACCCATTCAGCGTT 1483

Db 1484 TGAGAAATGGGAAAGTGAGCTCTGCTATATCGCGTAGCAACATTGCAACCCATCCTCACTT 1543

QY 1484 GGACATCCCCCTTCTCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543

Db 1544 GAATGCATGGCTTCTCTGATTACATCTTGAAGGAATTGATTTCCATCCAGTTCAATGA 1603

QY 1544 CTTGATATGTATCATCCTTCGATTAAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGC 1603

Db 1604 TTTGGCATCGTCTTCTTCCGTACGAGGTGACACACGCTGTCTACAAGGCCGATAGGGA 1663

QY 1604 CCGTGGAGAAAGCTTCGTCTATATCATGTTATATGAAAGACATCCTCGGATTAAACGA 1663

Db 1664 TCGTGGTGAAGAGCTTCGTGTATATCATGTTATATGAAAGACATCCTGGATCAACCGA 1723

QY 1664 AGAAGATGCTCTGAAATCATATCAACTTCATGATCAGGACGCAATCAGAGAATTAATTTG 1723

Db 1724 AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATATCAATCAAGAATTAATTTG 1783

QY 1724 GGAGCTTCTAAAAGCCAGACAACAGTGTTCCTCCATCACTTCCAAGAAACACGCAATTTGACAT 1783

Db 1784 GGAACCTTCTAAGATCCAACGACAATATTCCAATGCTGGCCAAAGAAACATGCTTTTGACAT 1843

QY 1784 AAGCAGAGTTTGGCATCACGGTTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843

Db 1844 ACAAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAAAGGA 1903

QY 1844 AACAAAGAGTTTGGTGATGAGAACCCGTCATTGAACCTGTGCTTGTGTAACAAACACTTCAA 1903

Db 1904 AACAAAAAATTGGTTATGGAAACACTCCTTGAATCTATGCTTTTTTAACTATAACCAT A 1963

QY 1904 ATCTACAAATTAATTAACCTGAGGATGCCCTATGGGTGTATATAGGGGACA 1950

Db 1964 TCCATAATAATAAGCTCATAATGCTAAATATATTTGGCCTTATGACATA 2010

Search completed: July 8, 2004, 17:14:45  
Job time : 1071.29 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:38:02 ; Search time 59 Seconds  
(without alignments)  
2959.565 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRSLSSSHE.....FANVETKSLVMRTVIEPVL 618

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	3251	100.0	618	4	AAB69390 Grand fir
2	2453	75.5	628	2	AAW85701 Pinene sy
3	2453	75.5	628	3	AAY90837 Grand fir
4	2453	75.5	628	4	AAB69371 Grand fir
5	2264	69.6	630	4	AAB69391 Grand fir
6	2200.5	67.7	627	2	AAW85700 Myrcene s
7	2200.5	67.7	627	3	AAY90842 Grand fir
8	2200.5	67.7	627	4	AAB69370 Grand fir
9	2197.5	67.6	627	2	AAW85710 Grand Fir
10	2197.5	67.6	627	4	AAB69380 Grand fir
11	2197.5	67.6	627	5	ABB79395 Taxadiene
12	2137	65.7	630	4	AAB69393 Grand fir
13	2084.5	64.1	637	4	AAB69392 Grand fir
14	2031.5	62.5	637	2	AAW85702 Limonene
15	2031.5	62.5	637	3	AAY90859 Grand fir
16	2031.5	62.5	637	4	AAB69372 Grand fir
17	1617.5	49.8	462	3	AAB18115 Pinus rad
18	1611.5	49.6	462	3	AAB18044 Pinus rad
19	1295.5	39.8	580	2	AAY06571 Delta-sel
20	1295.5	39.8	581	2	AAY06570 Delta-sel
21	1295.5	39.8	581	2	AAY06563 Grand fir
22	1295.5	39.8	581	3	AAY90854 Grand fir
23	1291.5	39.7	581	2	AAY06569 Delta-sel
24	1267.5	39.0	344	3	AAB18043 Pinus rad
25	1250.5	38.5	577	2	AAW85704 Grand Fir

26	1250.5	38.5	577	4	AAB69374	Aab69374 Grand fir
27	1240.5	38.2	862	2	AAW31655	Aaw31655 Pacific Y
28	1240.5	38.2	862	3	AAY90852	Aay90852 Yew taxad
29	1240.5	38.2	862	5	ABB79394	Abb79394 Taxadiene
30	1236.5	38.0	862	6	ABU09782	Abu09782 Pacific Y
31	1231	37.9	593	2	AAU06572	Aay06572 Gamma-hum
32	1231	37.9	593	2	AAU06564	Aay06564 Grand fir
33	1231	37.9	593	3	AAY90855	Aay90855 Grand fir
34	1230	37.8	593	2	AAU06573	Aay06573 Gamma-hum
35	1230	37.8	593	2	AAU06574	Aay06574 Gamma-hum
36	1188.5	36.6	817	2	AAU06566	Aay06566 Grand fir
37	1188.5	36.6	817	5	ABB79391	Abb79391 Taxadiene
38	1187	36.5	782	2	AAW85703	Aaw85703 Grand Fir
39	1187	36.5	782	3	AAY90853	Aay90853 Grand fir
40	1187	36.5	782	4	AAB69373	Aab69373 Grand fir
41	1187	36.5	782	5	ABB79392	Abb79392 Taxadiene
42	1187	36.5	817	2	AAU06567	Aay06567 E-alpha-b
43	1187	36.5	817	2	AAU06568	Aay06568 E-alpha-b
44	1187	36.5	817	2	AAU06562	Aay06562 Grand fir
45	1187	36.5	817	6	ABU09781	Abu09781 White fir

ALIGNMENTS

RESULT 1  
AAB69390  
ID AAB69390 standard; protein; 618 AA.  
XX  
AC AAB69390;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir monoterpene synthase protein fragment SEQ ID NO: 65.  
XX  
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
XX  
DR WPI; 2001-182782/18.  
DR N-PSDB; AAF73411.  
XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
PS Claim 7; Page 150-151; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
XX insect resistance on plants  
SQ Sequence 618 AA;









Db 354 SSCIATEPKHSAFRLGFAKCHLITVLDDIYDTFGTMDTELEFNEAVRRWNPSEKERLPE 413  
QY 402 YNKGVMVMVYHTVNEMARVAEKAQGRDTLNARQAWEACFDSYMQEAQKWIATGYLPTFEE 461  
Db 414 YNKEIYMALYEALTMAREAEKTQGRDTLNARKAWEVYLDSTYQEAQKWIASGYLPTFEE 473  
QY 462 YLENGKVSSAHRPCALQPILTLDIPFPDHIILKEVDFPSKINDLICIILRLRGDTRCYKAD 521  
Db 474 YLENAKVSSGHRAAALTPLLTDVPLPDDVLKGIDFPSFPNDLASSFLRLRGDTRCYKAD 533  
QY 522 RARGEAEASSICYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGHAF 581  
Db 534 RDRGEEASSICYMKDNPGLTEEDALNHINAMINDIIEKLNWELLKPDNSNIPMTARKHAY 593  
QY 582 DISRVVHHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618  
Db 594 EITRAFHQLYKYRDGFSVATQETKSLVRRTVLEPVPL 630

RESULT 6  
AAW85700  
ID AAW85700 standard; protein; 627 AA.  
XX  
AC AAW85700;  
XX  
DT 27-SEP-1999 . (first entry)  
XX  
DE Myrcene synthase of grand fir.  
XX  
KW Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal.  
XX  
OS Abies grandis.  
XX  
PN WO9902030-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014528.  
PR 11-JUL-1997; 97US-0052249P.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
PI Bohlmann J, Steele CL, Croteau RB;  
XX  
DR WPI; 1999-120396/10.  
DR N-PSDB; AAX08643.  
XX  
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. myrcene, limonene or pinene.  
XX  
PS Claim 12; Page 72-74; 121pp; English.  
XX

CC Nucleotide sequences encoding myrcene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by myrcene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal  
SQ Sequence 627 AA;

Query Match 67.7%; Score 2200.5; DB 2; Length 627;  
Best Local Similarity 68.1%; Pred. No. 9.1e-197;  
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALLSITPLVSRSL-----SSSHEIKALRRITPTLGI CRPGKSVAH SINCLTSVASTD 55  
Db 1 MALVSIPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTPSMSISLATAAPDD 60  
QY 56 SVQRRVGNHNLWDDDFIQSLISTPYGAPDYRERADRRLIGEVKDIMENFKSLEDGG--- 112  
Db 61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPYSQERAERLIVEVKKI-FNSMYLDDGRLMS 118  
QY 113 --NDLLQRLLLVDDVERLIGDRHFKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170  
Db 119 SFNDLMQRLWIVDSVERLGIARHFKEITSAIDYVRYWEENGIGCGRDSIVTDLNSTAL 178  
QY 171 GLRTRLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVMD 230  
Db 179 GFRTLRLHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYASLIAFPGEKVME 237  
QY 231 EAETFTSKYLREALQKIPASSILSLEIRDVLEYGHTNLPRLARNYMDVFGQHTK---N 287  
Db 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGHTNLPRLARNYIDTLEKDTSAWLN 296  
QY 288 KNAAEKLLLELAKLEFNIFHSLQERELKHVSRWWDKSGSPEMTFCRHRHVEYVALASCI AF 347  
Db 297 KNAGKKLLELAKLEFNIFNSLQOKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI AF 356  
QY 348 EPQHSGLFRLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407  
Db 357 DPKHSAFRLGFAKMCHLVTVLDDIYDTFGTIDELELFTSAIKRWNSSEIEHLPYMKCVY 416  
QY 408 MMVYHTVNMARVAEKAQGRDTLNARQAWEACDSYMQEAKWIATGYLPTFEEYLENGK 467  
Db 417 MVVFETVNLTREAEKTQGRNTLNYYVRKAWEAYFDSYMEEAKWISNGYLPMEFEYHENGK 476  
QY 468 VSSAHRPCALQPILTLDIPFPDHIILKEVDFPSKINDLICIILRLRGDTRCYKADRARGE 527  
Db 477 VSSAYRVATLQPILTNLAWLPDYILKGIDFPSRFPNDLASSFLRLRGDTRCYKADRDRGE 536  
QY 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVW 587  
Db 537 ASCISCYMKDNPGSTEEEDALNHINAMVNDIIEKLNWELLRSNDNIPMLAKKHAFDITRAL 596  
QY 588 HHGYRYRDGYSFANVETKSLVMRTVIE 614  
Db 597 HHLIYIRDGFSVANKETKKLVMETLLE 623

RESULT 7  
AAV90842  
ID AAV90842 standard; protein; 627 AA.  
XX  
AC AAV90842;

DT 25-AUG-2000 (first entry)

XX Grand fir myrcene synthase protein sequence SEQ ID NO:30.

DE  
XX  
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;  
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;  
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;  
KW defensive agent; pigment; antitumour; steroid hormone;  
KW signal transduction pathway; bile acid; affinity purification;  
KW photoreceptor; enzymatic synthesis; nutrient supplement;  
XX immunological reagent.

OS Abies grandis.

XX WO200017327-A2.

PN 30-MAR-2000.

XX 17-SEP-1999; 99WO-US021419.

XX 18-SEP-1998; 98US-0100993P.

PR 22-APR-1999; 99US-0130628P.

PR 23-AUG-1999; 99US-0150262P.  
XX (KENT ) UNIV KENTUCKY RES DEPT.  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX Chappell J, Manna KR, Noel JP, Starks CM;  
PI  
XX WPI; 2000-292839/25.  
DR N-PSDB; AAA38927.  
DR  
XX Novel terpene synthase enzymes, useful for producing terpene  
PT hydrocarbons, e.g. fragrances or anticumor agents, are derived from known  
PT enzymes by specific amino acid alterations.  
XX  
PS Claim 117; Page 390-392; 450pp; English.  
XX  
CC The present invention describes an isolated terpene synthase (I)  
CC comprising a region with at least 20% identity to region 265-535 of a 548  
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha  
CC -carbon atoms (alphaC) that have interatomic distances, between each  
CC other, within tabulated ranges, have a centre point (within a sphere of  
CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered  
CC arrangement of R groups (defining aa side chains), excluding specific  
CC tabulated arrangements (tables given in the specification). (I), and  
CC related enzymes, are used to produce a wide range of terpenoids (e.g.  
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,  
CC flavours, pheromones, defensive agents, pigments, antitumour agents,  
CC components of signal transduction pathways, precursors of steroid  
CC hormones and bile acids, as photoreceptors and as co-factor side chains.  
CC Some synthases with little or no catalytic activity (and nucleic acids  
CC encoding them) are used as controls in the analysis of products formed by  
CC enzymatic synthesis; as nutrient supplements; for affinity purification  
CC of isoprenoids; or to develop immunological reagents or nucleic acids for  
CC monitoring expression of terpene synthase or inheritance of the gene in  
CC plant breeding programs. The new synthases may produce novel terpene  
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 627 AA;

Query Match 67.7%; Score 2200.5; DB 3; Length 627;  
Best Local Similarity 68.1%; Pred. No. 9.1e-197;  
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALLSITPLVRSCL-----SSSHEIKALRRRTIPTIGICRPGKSVAHNSINMCLTSVASTD 55  
DB 1 MALVSIPLASKSCLRSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60  
QY 56 SVQRRVGNHNSLWDDDFIQSLSTPYGAPDYRERADRRLIGEVDKIMFNFKSLEDGG--- 112  
DB 61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPSPYQERARRLIVEVKKI-FNSMYLDDGR LMS 118  
QY 113 --NDLLQRLLLVDDVERLIGDRHFKEIKTALDYVNSYWNKGI GCGRESVVTDLNSTAL 170  
DB 119 SFNDLMQRLWI VDSVERLGIARHFKN EITSA LDYVFRYWEENGIGCGRDSIVTDLNSTAL 178  
QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGIRGVNLNLFRA SLVAFPGKVM D 230  
DB 179 GFRTLRLHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLNLYRASLIAFP GKVME 237  
QY 231 EAETFSTKYLREALQKIPASSILSLEIRDVLEYGWHNLPRLEARNYMDVFGQHTK---N 287  
DB 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGWHNLPRLEARNYIDTLEK DTSAWLN 296  
QY 288 KNAAEKLLLELAKLEFNIFHSIQERELKHVSRWVKDSGSPBMTFCRRHRHVEYYALASCI AF 347  
DB 297 KNAGKKLLELAKLEFNIFNSIQQKELQYLLRWKESDLPKLTFA RHRHVEFYTLASCI AI 356  
QY 348 EPOHSGFRGLGFTKMSHLITVLDMDYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407  
DB 357 DPKHSAFRLGFAKMCHLVTVLDDIYDTFGTIDELELFTSAIKRWNSS EIEHLPEYMKCVY 416  
QY 408 MMVYHTVNMARVAEKAQGRDITLNYARQAWAEACFDSYMQEAKW IATGYLPTTFEEYLENGK 467

DB 417 MVVFETVNELTREAEKTQGRNTLNYVRKAWEAYFDSYMEEAKWISNGYLP MFEEYHENGK 476  
QY 468 VSSAHRPCALQPILTDIPFPDHILKEVDPPSKLNDLICIIILRLRGDTRCYKADRARGE E 527  
DB 477 VSSAYRVATLQPILTLNWLFDYILKGIDFPFRFNDLASSFLRLRGDTRCYKADRDREE 536  
QY 528 ASSISCYMKDNPGLTEEDALNHINFMIRDALRELNWELLKPDNSVPITSKKHAFDISRVW 587  
DB 537 ASCISCYMKDNPGSTEEDALNHINAMVNDI IKELNWE LLRSNDNIPMLAKKHAFDITRAL 596  
QY 588 HHGYRYRDGYSPANVETKSLVMRTVIE 614  
DB 597 HHLYIYRDGFSVANKETKKLVMETLLE 623

RESULT 8  
AAB69370  
ID AAB69370 standard; protein; 627 AA.  
XX  
AC AAB69370;  
XX 30-APR-2001 (first entry)  
XX Grand fir myrcene synthase SEQ ID NO: 2.  
DE Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
XX myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition.  
KW Abies grandis.  
XX WO200107565-A2.  
XX 01-FEB-2001.  
XX 24-JUL-2000; 2000WO-US020264.  
XX 26-JUL-1999; 99US-00360545.  
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
PA Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
XX WPI; 2001-182782/18.  
DR N-PSDB; AAF73371.  
XX New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX Claim 58; Page 106-107; 175pp; English.  
PS The present invention provides the protein and coding sequences of  
XX monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 627 AA;

Query Match 67.7%; Score 2200.5; DB 4; Length 627;  
Best Local Similarity 68.1%; Pred. No. 9.1e-197;  
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALLSITPLVRSCL-----SSSHEIKALRRRTIPTIGICRPGKSVAHNSINMCLTSVASTD 55  
DB 1 MALVSIPLASKSCLRSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60  
QY 56 SVQRRVGNHNSLWDDDFIQSLSTPYGAPDYRERADRRLIGEVDKIMFNFKSLEDGG--- 112



XX Grand fir monoterpene synthase protein fragment SEQ ID NO: 32.  
DE  
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition.  
XX  
OS Abies grandis.  
XX  
XX WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
XX 24-JUL-2000; 2000WO-US020264.  
XX  
XX 26-JUL-1999; 99US-00360545.  
XX  
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
XX Steele CL, Bohlmann J, Croteau RB, Phillips MA;  
XX  
XX WPI; 2001-182782/18.  
DR N-PSDB; AAF73391.  
XX  
XX New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
XX Disclosure; Page 138-139; 175pp; English.  
XX  
XX The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
XX Sequence 627 AA;

Query Match 67.6%; Score 2197.5; DB 4; Length 627;  
Best Local Similarity 68.1%; Pred. No. 1.7e-196;  
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALLSITPLVRSCL-----SSSHEIKALRRITPIIGICRPGKSAHNSINMCLTSVASTD 55  
DB 1 MALVSIPLASKSLRSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60  
QY 56 SVQRRVGNYSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDKIMFNFKSLDDGG--- 112  
DB 61 GVQRRIGDYHSNIWDDDFIQSL-STHYGEPYQERAEERLIVEVKI-FNSMYLDDGRLMS 118  
QY 113 --NDLLQRLLLVDDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170  
DB 119 SFNDLMQRLWIVDSVERLGIARHFKNIEITSALDYVPYWEENGIGCGRDSIVTDLNSTAL 178  
QY 171 GLRTLRLHGYTVSSDVNLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFGEKVMVD 230  
DB 179 GFRTLRLHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYRASLIAFGEKVME 237  
QY 231 EAETFTSKYLREALQKIPASSILSLEIRDVLEYGHTNLPRLRNMYMDVFGQHTK---N 287  
DB 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGHNTNLPRLRNMYIDTLEKDTSAWLN 296  
QY 288 KNAAEKLLLELAKLEFNIHSLQERELKHVSRWWKDSGSPENTFCRRHRHVEYYALASCIAP 347  
DB 297 KNAGKKLLELAKLEFNIHSLQERELKHVSRWWKDSGSPENTFCRRHRHVEYYALASCIAP 356  
QY 348 EPQHSGRFLGFTKMSHLITVLDMDYDVFVGTVDLELFTATIKRWDPSPAMECLPEYMKGVY 407  
DB 357 DPKHSAFRLGFAKMCMLVTVLDDIYDTFTGTIDELELFTSAIKRWNSSSEIEHLPEYMKCVY 416

QY 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAWAEACFDSYMQEAKWIATGYLPTFEEYLENGK 467  
DB 417 MVVFETVNELTREAEKTOGRNTLNYVRKAWAEAYFDSYMEEAKWISNGYLPTEFEEYHENGK 476  
QY 468 VSSAHRPCALQPIILTDIPFPDHLKEVDFPSKLNLDLICIILRLRGDTRCYKADRARGE 527  
DB 477 VSSAYRVATLQPIILTNLAWLPDYILKGIDFPSPRFNDLASSFLRLRGDTRCYKADRDRGE 536  
QY 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVW 587  
DB 537 ASCISCYMKDNPGSTEEEDALNHINAMVNDIIEKLNWELLRSNDNIPMLAKKHAFDITRAL 596  
QY 588 HHGYRYRDGYSFANVETKSLVMRTVIE 614  
DB 597 HHLYIYRDGFSVANKETKLVMETLLE 623  
RESULT 11  
ABB79395  
ID ABB79395 standard; protein; 627 AA.  
XX  
AC ABB79395;  
XX  
DT 13-AUG-2002 (first entry)  
XX  
DE Taxadiene synthase homologous protein sequence w85710.  
XX  
KW Taxane; taxane synthesis; taxadiene synthase; cytostatic; anticancer;  
KW enzyme.  
XX  
OS Unidentified.  
XX  
PN WO200240694-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 16-NOV-2001; 2001WO-DK000763.  
XX  
PR 17-NOV-2000; 2000DK-00001730.  
PR 29-NOV-2000; 2000US-0253843P.  
XX  
PA (NOVO ) NOVOZYMES AS.  
XX  
PI Vind J;  
XX  
DR WPI; 2002-471624/50.  
XX  
PT Heterologous production of taxane analogs related compound useful as  
PT anticancer agent involves cloning a full-length taxane synthesis pathway  
PT from a taxan-producing organism into a taxane-resistant host cell.  
XX  
PS Example 3; Fig 1; 60pp; English.  
XX  
CC The present invention describes the heterologous expression of taxane  
CC analogues, comprising cloning a DNA sequence comprising a taxane  
CC synthesis pathway, making a DNA construct in which the DNA sequence is  
CC under control of regulatory elements, introducing the DNA construct into  
CC a host cell, growing the host cell to produce taxane analogues, and  
CC recovering the required taxane from the culture medium. Also described:  
CC (1) an isolated DNA sequence comprising the taxane synthesis pathway,  
CC (preferably taxol synthesis pathway); (2) an expression vector comprising  
CC the isolated DNA sequence; and (3) a host cell comprising a taxane  
CC synthesis pathway derived from a taxane-producing organism, plant or  
CC tree, the taxane synthesis pathway is foreign to the host cell. The  
CC taxane analogues have cytostatic activity, and so can be used as  
CC anticancer agents. The present sequence represents a taxadiene synthase  
CC homologous protein, which is given in an example from the present  
CC invention  
XX  
SQ Sequence 627 AA;

Query Match 67.6%; Score 2197.5; DB 5; Length 627;  
Best Local Similarity 68.1%; Pred. No. 1.7e-196;







Matches 409; Conservative 84; Mismatches 119; Indels 31; Gaps 14;

QY 1 MALLSITPL-VSRSC-----LSSSHEIKAL--RRTIPTLGICRPGKSVAHSNMCLTSVA 52  
||||| | | | | : ||| : ||| : | | : | | | | : | | :  
Db 1 MALLSIVSLQVPKSCGLKSLISSNVQKALCISTAVPTLRMRRRQKALV--INMKLTTVS 58

QY 53 STDS-----VQRRVGNVHSNLWDDDFIQSLISTPYGADPYRERADRLLIGEVDIMFNF-- 105  
| : ||| : : | | | | | | | | | | | | | | | | | | : | | | |  
Db 59 HRDDNGGGVLQRRRIADHHPNLWEDDFIQSL-SSPYGGSSYSERAETVVEEVKE-MFNSIP 116

QY 106 --KSLEDGGNDLLQRLLLVDDVERLIGIDRHFKEIKTALDYVNSYWNK-GIGCGRESV 162  
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 117 NNRELFGSQNDLLTRLWMVDSIERLIGIDRHFQNEIRVALDYVYSYWKKEGIGCGRDSTF 176

QY 163 TDLNSTALGLRTLRLHGYTVSSDVNLVFKDKNGQFSSTANIQIEGEI-RGVNLFRASLV 221  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 177 PDLNSTALALRTLRLHGVNVSSDVLEFYFDEKGFACPA-ILTEGQITRSVLNLYRASLV 235

QY 222 AFPGEKVMDEAETFTSKYLREALQKIPASSILSLIIRDVLEYGWHTNLPRLARNYMDVF 281  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 236 AFPGEKVMEEAEIFSASYLKKVLQKIPVSN-LSGEIEYVLEYGWHTNLPRLARNYIEVY 294

QY 282 ---GOHTKNKNA---AEKLLLELAKLEFNIFHSLQERELKHVSRWVKDSGSPMTFCRHRH 335  
| : | : : | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 295 EQSGYESLNEMPYMNMKLLQLAKLEFNIFHSLQRELQSISSRWKESGSSQLTFTTRHRH 354

QY 336 VEYYALASCIAPFEPQHSGRFLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSA 395  
||||| : |||| : | | | | | | | | | | | | | | | | | | | | | | |  
Db 355 VEYYTMASCIISMLPKHSAFRMBFVKVCHLVTVLDDIYDTFGTMNELQLFTDAIKRWDLST 414

QY 396 MECLPEYMKGVMMVYHTVNMARVAEKAQGRDITLNYARQAWAEACFDSYMOBAKWIATGY 455  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 415 TRWLPEYMKGVMDLYQCINEMVEEAEKTOGRDMLNVIQNAWEALFDTFQEAKWISSY 474

QY 456 LPTFEEYLENGKVSSAHRPCALQPILTLDPDPDHILKEVDFPSKLNLDLICIILRLRGDT 515  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 475 LPTFEEYLNKARVSSGSRIATLQPILTLDPDPDYILQEIIDYPSRFNELASSILRLRGDT 534

QY 516 RCYKADRARGEAEASSISCYMKDNPGLTTEEDALNHINFMIRDIAIRELNWELLKPDNSVPIT 575  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 535 RCYKADRARGEAEASISCYMKDHPGSIIEEDALNHINAMISDAIRELNWELLRPDSKSPIS 594

QY 576 SKKHAFDISRVWHGYRYRDGYSEFANVETKSLVMRTVIEPVPL 618  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 595 SKKHAFDITRAFHVHYKYRDGYTVSNNETKNLVMKTVLEPLAL 637

RESULT 15  
AAY90859  
ID AAY90859 standard; protein; 637 AA.

XX AAY90859;  
AC  
XX  
DT 25-AUG-2000 (first entry)  
XX  
DE Grand fir limonene synthase protein sequence SEQ ID NO:58.  
XX  
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;  
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;  
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;  
KW defensive agent; pigment; antitumour; steroid hormone;  
KW signal transduction pathway; bile acid; affinity purification;  
KW photoreceptor; enzymatic synthesis; nutrient supplement;  
KW immunological reagent.

XX Abies grandis.  
XX  
XX WO200017327-A2.  
XX  
XX  
PD 30-MAR-2000.  
XX  
XX  
PF 17-SEP-1999; 99WO-US021419.  
XX

PR 18-SEP-1998; 98US-0100993P.  
PR 22-APR-1999; 99US-0130628P.  
PR 23-AUG-1999; 99US-0150262P.  
XX  
PA (KENT ) UNIV KENTUCKY RES DEPT.  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Chappell J, Manna KR, Noel JP, Starks CM;  
XX  
DR WPI; 2000-292839/25.  
DR N-PSDB; AAA38938.  
XX  
PT Novel terpene synthase enzymes, useful for producing terpene  
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known  
PT enzymes by specific amino acid alterations.  
XX  
PS Claim 104; Page 448-450; 450pp; English.  
XX  
CC The present invention describes an isolated terpene synthase (I)  
CC comprising a region with at least 20% identity to region 265-535 of a 548  
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha  
CC -carbon atoms (alphaC) that have interatomic distances, between each  
CC other, within tabulated ranges, have a centre point (within a sphere of  
CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered  
CC arrangement of R groups (defining aa side chains), excluding specific  
CC tabulated arrangements (tables given in the specification). (I), and  
CC related enzymes, are used to produce a wide range of terpenoids (e.g.  
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,  
CC flavours, pheromones, defensive agents, pigments, antitumour agents,  
CC components of signal transduction pathways, precursors of steroid  
CC hormones and bile acids, as photoreceptors, and as co-factor side chains.  
CC Some synthases with little or no catalytic activity (and nucleic acids  
CC encoding them) are used as controls in the analysis of products formed by  
CC enzymatic synthesis; as nutrient supplements; for affinity purification  
CC of isoprenoids; or to develop immunological reagents or nucleic acids for  
CC monitoring expression of terpene synthase or inheritance of the gene in  
CC plant breeding programs. The new synthases may produce novel terpene  
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 637 AA;

Query Match 62.5%; Score 2031.5; DB 3; Length 637;  
Best Local Similarity 63.6%; Pred. No. 6.6e-181;  
Matches 409; Conservative 84; Mismatches 119; Indels 31; Gaps 14;

QY 1 MALLSITPL-VSRSC-----LSSSHEIKAL--RRTIPTLGICRPGKSVAHSNMCLTSVA 52  
||||| | | | | : ||| : ||| : | | : | | | | : | | :  
Db 1 MALLSIVSLQVPKSCGLKSLISSNVQKALCISTAVPTLRMRRRQKALV--INMKLTTVS 58

QY 53 STDS-----VQRRVGNVHSNLWDDDFIQSLISTPYGADPYRERADRLLIGEVDIMFNF-- 105  
| : ||| : : | | | | | | | | | | | | | | | | | | : | | | |  
Db 59 HRDDNGGGVLQRRRIADHHPNLWEDDFIQSL-SSPYGGSSYSERAETVVEEVKE-MFNSIP 116

QY 106 --KSLEDGGNDLLQRLLLVDDVERLIGIDRHFKEIKTALDYVNSYWNK-GIGCGRESV 162  
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 117 NNRELFGSQNDLLTRLWMVDSIERLIGIDRHFQNEIRVALDYVYSYWKKEGIGCGRDSTF 176

QY 163 TDLNSTALGLRTLRLHGYTVSSDVNLVFKDKNGQFSSTANIQIEGEI-RGVNLFRASLV 221  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 177 PDLNSTALALRTLRLHGVNVSSDVLEFYFDEKGFACPA-ILTEGQITRSVLNLYRASLV 235

QY 222 AFPGEKVMDEAETFTSKYLREALQKIPASSILSLIIRDVLEYGWHTNLPRLARNYMDVF 281  
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 236 AFPGEKVMEEAEIFSASYLKKVLQKIPVSN-LSGEIEYVLEYGWHTNLPRLARNYIEVY 294

QY 282 ---GOHTKNKNA---AEKLLLELAKLEFNIFHSLQERELKHVSRWVKDSGSPMTFCRHRH 335  
| : | : : | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 295 EQSGYESLNEMPYMNMKLLQLAKLEFNIFHSLQRELQSISSRWKESGSSQLTFTTRHRH 354

QY 336 VEYYALASCIAPFEPQHSGRFLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSA 395  
||||| : |||| : | | | | | | | | | | | | | | | | | | | | | | |  
Db 355 VEYYTMASCIISMLPKHSAFRMBFVKVCHLVTVLDDIYDTFGTMNELQLFTDAIKRWDLST 414

Qy 396 MECLPEYMKGVMMVYHTVNEMARVAEKAQGRDRTLNYARQAWAEACFDSYMQEAKWIATGY 455  
Db 415 TRWLPEYMKGVYMDLYQCINEMVEEAETQGRDMLNYIQNAWEALFDTFMQEAKWISSY 474  
Qy 456 LPTFEEYLENGKVSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNLDLICIILRLRGDT 515  
Db 475 LPTFEEYLNKAKVSSGSRIATLQPILTLDVPLPDYILQEIDYPSRFNELASSILRLRGDT 534  
Qy 516 RCYKADRARGEAEASSISCYMKDNPGLTEEDALNHINFMIRDARELNWELLKPDNSVPIT 575  
Db 535 RCYKADRARGEAEASISCYMKDHPGSTEEDALNHINAMISDAIRELNWELLRPDSKSPIS 594  
Qy 576 SKKHAFDISRVWHHGYRYRDGYSEFANVETKSLVMRTVIEPVPL 618  
Db 595 SKKHAFDITRAFHVYKYRDGYTVSNNETKNLVMKTVLEPLAL 637

Search completed: July 7, 2004, 17:42:14  
Job time : 61 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:40:02 ; Search time 21 Seconds  
(without alignments)  
2830.779 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRSLSSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					% Match		Query Match		Length DB ID		Description	
Result No.	Score	Match	Length	DB ID								
1	724.5	22.3	599	2	A48863						limonene cyclase -	
2	717.5	22.1	554	2	S68366						(+)-delta-cadinene	
3	717.5	22.1	554	2	S68365						(+)-delta-cadinene	
4	689.5	21.2	591	2	H84633						probable limonene	
5	669.5	20.6	520	2	A56118						vetispiradiene syn	
6	656	20.2	600	2	F71434						probable limonene	
7	641.5	19.7	550	2	T03714						5-epi-aristolochene	
8	632	19.4	559	2	T08174						sesquiterpene cycl	
9	615.5	18.9	548	2	T06266						germacrene C synth	
10	614.5	18.9	548	2	T06265						germacrene C synth	
11	586.5	18.0	1024	2	G71434						probable limonene	
12	569	17.5	632	2	E96723						hypothetical prote	
13	536	16.5	598	2	H86460						hypothetical prote	
14	504.5	15.5	785	2	G96825						hypothetical prote	
15	504.5	15.5	785	2	T52059						ent-kaurene syntha	
16	497.5	15.3	608	2	G86443						probable terpene s	
17	486.5	15.0	789	2	T09672						ent-kaurene syntha	
18	483	14.9	582	2	C71424						hypothetical prote	
19	481	14.8	530	2	G96588						hypothetical prote	
20	437.5	13.5	598	2	T00509						probable vetispira	
21	427.5	13.1	421	2	C96642						hypothetical prote	
22	426	13.1	598	2	F96684						probable terpene s	
23	425	13.1	350	2	C56118						vetispiradiene syn	
24	423.5	13.0	801	2	T06783						ent-kaurene syntha	
25	415.5	12.8	573	2	T05328						hypothetical prote	
26	408	12.5	802	2	D85035						ent-kaurene synthe	
27	406.5	12.5	612	2	T05331						hypothetical prote	
28	405	12.5	870	2	A96637						hypothetical prote	
29	404.5	12.4	823	2	T02959						kaurene synthase A	

30	404	12.4	383	2	D71424	hypothetical prote
31	401	12.3	535	2	T06285	hypothetical prote
32	393.5	12.1	598	2	T05329	hypothetical prote
33	359.5	11.1	300	2	B56118	vetispiradiene syn
34	320.5	9.9	471	2	T06287	hypothetical prote
35	185.5	5.7	203	2	H96525	probable terpene c
36	133	4.1	1941	2	T30554	ubiquitin-protein
37	125	3.8	1296	2	I40645	botulinum neurotox
38	120.5	3.7	942	2	B72015	metalloproteinas,
39	120.5	3.7	942	2	C86610	insulinase family/
40	120	3.7	834	2	T19010	hypothetical prote
41	119.5	3.7	1077	2	A97306	superfamily II DNA
42	117.5	3.6	1187	2	JE0347	hypothetical prote
43	117.5	3.6	1493	2	A38218	GAP-associated pro
44	116	3.6	456	2	AG0199	adenylosuccinate 1
45	116	3.6	576	2	AC1384	phosphomannomutase

ALIGNMENTS

RESULT 1

A48863

limonene cyclase - spearmint

C;Species: Mentha spicata (spearmint)

C;Date: 12-May-1995 #sequence\_revision 19-May-1995 #text\_change 05-Nov-1999

C;Accession: A48863

R;Colby, S.M.; Alonso, W.R.; Katahira, E.J.; McGarvey, D.J.; Croteau, R.

J. Biol. Chem. 268, 23016-23024, 1993

A;Title: 4S-limonene synthase from the oil glands of spearmint (Mentha spicata). cDNA iso

A;Reference number: A48863; MUID:94043077; PMID:8226816

A;Accession: A48863

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-599 <COL>

A;Cross-references: GB:L13459; NID:g410229; PIDN:AAC37366.1; PID:g410230

C;Superfamily: vetispiradiene synthase 1

Query Match 22.3%; Score 724.5; DB 2; Length 599;  
Best Local Similarity 31.7%; Pred. NO. 4.1e-43;  
Matches 197; Conservative 114; Mismatches 249; Indels 61; Gaps 16;

QY	13	SCLSSSHEIKALRRTIPTLGICRPGKSVAHNSINMCLTSTVASTDSVQRVGVNHSNLWDDD	72
Db	20	TCLQPSH----FKSSPKLLSSTNSSRSRLRVYCSSLT---ERSGNYNPSRWDVN	71
QY	73	FIQSLISTPYGAPDYRE----RADRLIGEVDIMFNFKSLEDGGNDLQRLLLVDDVER	127
Db	72	FIQSLLS-----DYKEDKHVIRASELVTLVK-----MELEK-ETDQIRQLELIDDLQR	118
QY	128	LGIDRHFKEIKTAID-----YVNSYWNKEGIGCGRESVVTDLNSTALGLRTLRLHG	179
Db	119	MGLSDHFQNEFKEILLSSIIYLDHHYKKNPFPKBE-----RDLYSTSLAFRLREHG	168
QY	180	YTVSSDVLVNFKDNGQFSSTANIQIEGEIRGVNLFRASLVAFPGEKVMDEAETFSTKY	239
Db	169	FQVAQEVFDSFKNEEGEFKES---LSDDTRGLLQLYEASFLLTEGETTLESAREFATKF	224
QY	240	LREALQKIPASSILSLEIRDVLEYGWHTNLPRLEARNYMDVFGQHTKNKNAAEKLLLELAK	299
Db	225	LEEKVNEGVDGDLTRIAYSLDIPLHWRIKRPNAPVWIE---WYRKRPDMNPVVLLEAI	281
QY	300	LEFNIFHSLQERELKHVSRWWKDSGSPE-MTFCRHRHVEYYALASCIAPFQHSGRIGF	358
Db	282	LDLNIVQAQFQEELKESFRWRNTGFEVKLPFARDRLVECYFNTGIIEPRQHASARIMM	341
QY	359	TKMSHLITVLDMDYVFGTVDELELFTATIKRWDPSPAMECLPEYMKGVMMVYHTVNEMA	418
Db	342	GKVNALITVIDDIYDVYGTLEELEQFTDLIRRDINSIDQLPDYMQLCFLALNNFVDDTS	401
QY	419	RVAEKAQGRDITLYARQAEACFDSYMQEAKWIATGYLPTFEEYLENGKVSSAHRPCALQ	478
Db	402	YDVMEKGVNVIPLYLRQSWVDLADKYMVEARWFYGGHKPSLEEYLEN-SWQSIISGPCMLT	460

QY	479	PILTLDIPFPDHILKE-VDFPSKLNDLI---- <td>534</td>	534
Db	461	HIF---FRVTDSTFKETVDSLKYHDLVRWSSFVLRLADDLGTSVEEVSRGDVPKSLQCY	517
QY	535	MKDNPLTEEDALNHINEMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVWHHGYYR	594
Db	518	MSDY-NASEAEARKHVKWLLTAETVWKKNNAERVSKDSPFGKDFIGCAVDLGRMAQLMYHNG	576
QY	595	DGYSFANVETKSLVMRTVIEP	615
Db	577	DGHGTOHPPIIHOOMTRILFEF	597

RESULT 2  
S68366  
(+)-delta-cadinene synthase isozyme XC14 - *Gossypium arboreum*  
C;Species: *Gossypium arboreum*  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 29-Sep-1999  
C;Accession: S68366  
C;Chen, X.Y.; Chen, Y.; Heinsteins, P.; Davisson, V.J.  
Arch. Biochem. Biophys. 324, 255-266, 1995  
A;Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat  
A;Reference number: S68365; MUID:96132653; PMID:8554317  
A;Accession: S68366  
A;Molecule type: mRNA  
A;Residues: 1-554 <CHE>  
A;Cross-references: EMBL:U23205; NID:g1045313; PIDN:AAA93065.1; PID:g1045314  
A;Experimental source: cultivar Nanking  
C;Superfamily: vetispiradiene synthase 1  
C;Keywords: phytoalexin biosynthesis

Query Match	22.1%;	Score	717.5;	DB	2;	Length	554;
Best Local Similarity	31.9%;	Pred.	No. 1.1e-42;				
Matches	184;	Conservative	108;	Mismatches	241;	Indels	43;
Gaps	14;						
QY	51	VASTDSVQRRVGNVYHNSLWDDDFIQSLISTPYGAPD-----YRERADRLIGEVKDIMFN	104				
DB	14	LSSNKDEMRPKADFQPSIWGDLFL-----NCPDKNIDAETEKRHQQLKBEVR-----	60				
QY	105	FKSLEDGGNDLLQRLLLVDDVERLGIDRHFKEIKTALDVNSYWNKEGIGCGRESVVTD	164				
DB	61	-KMIVAPMANSTOKLAFIDSVQRLGVSYHFTKEIDELE--NIYHN-----NND AEND	110				
QY	165	INSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFP	224				
DB	111	LYTTSRLFRLLREHGPNVSCDVFNFKEQGNFKSS-----VTS DVRGLLELYQASYLRVH	166				
QY	225	GEKVMDEAETFTKYVIREALQKIPASSILSLEIRDVLEYGWHNTLPRLEARNYMDVFGQH	284				
DB	167	GEDILDEAISFTTNHLSLAVASLDYP--LSEEVSHALKQSIRRLPRVEARHVL SVY-QD	223				
QY	285	TKNKNAAEKLLEAKLEFNI FHSLOERELKHVSRWKD-SGSPEMTFCRHRHVEYYALAS	343				
DB	224	IESHN--KVLEFAKIDFNMVQLLHRKELSEISRWWKDLDFQRKLPYARDRVVGEYFWIS	281				
QY	344	CIAFEPQHSGFGLFTKMSHLITVLDDMYDVGTVDEBELFTATIKRWDPSAMECLPEYM	403				
DB	282	GVYFEPQYSLGRKMLTKVIAMASIVDDTYDSYATVEELIPYTKAIERWDIKCIDELPEYM	341				
QY	404	KGVMVMVYHTVNEMARVAEKAQGRDITLNYARQAEACFDSYMQEA KWIATGYLPTFEYL	463				
DB	342	KPSYKALLDVYEEMEQLVAKHGRQYRVEYAKNAMIRLAQSYLVEARWTLQNYKPSFEFK	401				
QY	464	ENGKVSSAHRPCALQPI LTL-DIPFPDHILKEVDFPSKINDLICII LRLRGDTRCYKADR	522				
DB	402	ANALPTCGYAMLAITSVFGMGDIVTPETFKWAANDP-KIIQASTIICRFMDDVAEHKFKH	460				
QY	523	ARGEAEASSISCYMKONPGLTEEDALNHINFMIRDAIRLKNWELLKPDNSVPITSKKHPD	582				
DB	461	RREDDCSAIECYMEEY-GVTAQEA YDVFNKHVESAWKDVNKEFLKP-TEMPTEVLNRS LN	518				
QY	583	ISRYVWHGYYR YRDGYGSFANVETKSLVMRTVIEPVPL	618				

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Db      519 LARVMDVLXREGDGYTVVGKAAKGGITSLLEPVAL 554
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RESULT 3
S68365 (+)-delta-cadinene synthase isozyme XC1 - Gossypium arboreum
C;Species: Gossypium arboreum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C;Accession: S68365
R;Chen, X.Y.; Chen, Y.; Heinstein, P.; Davison, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A;Title: Cloning, expression, and characterization of (+)-delta-cadinene sy
A;Reference number: S68365; MUID:96132653; PMID:8554317
A;Accession: S68365
A;Molecule type: mRNA
A;Residues: 1-554 <CHE>
A;Cross-references: EMBL:U23206; NID:g1045311; PIDN:AAA93064.1; PID:g104531
A;Experimental source: cultivar Nanking
C;Superfamily: vetispiradiene synthase 1
C;Keywords: phytoalexin biosynthesis
```

RESULT 4  
H84633  
probable limonene cyclase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C;Accession: H84633

R.;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84633

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-591 <STO>

A;Cross-references: GB:AE002093; NID:g4115381; PIDN:AAD03382.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g24210

A;Map position: 2

C;Superfamily: vetispiradiene synthase 1

Query Match 21.2%; Score 689.5; DB 2; Length 591;  
Best Local Similarity 29.3%; Pred. No. 1.2e-40;  
Matches 182; Conservative 130; Mismatches 238; Indels 71; Gaps 19;

QY 23 ALRRTIPTLGICRPGKSAHSINMCL-----TSVASTDSVQRRVGNVHNSLWDDDFIQSL 77  
Db 16 ALRKTLR-----RQSSST-----CIIVTETTPCNKSPVQRRSANYQPSRWDHHLHSV 64  
QY 78 ISTPYGAPDYRERADRLIGEVDIMFNFKSLDGGNDLLQRLLLVDDVERLIGDRHFKE 137  
Db 65 ENKFAKDKRVRR-DLLKEKVR-----KMLNDEQKTYLDQLEFIDDLQKLGVSYHFEAE 117  
QY 138 IKTALDVNSYNWKEGICGGRSVVTDLNSTALGLRTLRLHGTVSSDVLNVFKDKNGQF 197  
Db 118 IDNIL--TSSYKKDR-----TNIQESDLHATALEFRLFRQHGFNVSEDFVFMENCCKF 170  
QY 198 SSTANIQIEGEIRGVNLFRASLVAFPGKVM-D-EAETFSTKYLREALQKIPASSILSLE 256  
Db 171 D-----RDDIYGLISLYEASYLSTKLDKNLQIFIRPFATQQLRDFVTHSNEDFGSCD 223  
QY 257 IRDV----LEYGHTNLPRLARNYMDVFGQHTKNNAEKLLELAKLEFNIFHSLQERE 312  
Db 224 MVEIVVQALDMPYVQMRRLSTRWYIDVYGRQYKNLV--VVEFAKIDFNIVQAIHQEE 281  
QY 313 LKHVSRWVKDSC-SPMTFCRHRHVEYYALASCIAPFQHSGRFLGFTKMSHLITVLDDM 371  
Db 282 LKNVSSWMMETGLGKQLYFARDRIVENYFWTIGQIEPQYGYVRQVTMTKINALLTTIDDI 341  
QY 372 YDVGTVDELELFTATIKRWDPDSAMECLPEVMKGVMMVYHTVNMARVAEKAQGRDTLN 431  
Db 342 YDIYGTLEELQLFTVAFENWDINRLDELPEYMRCLFLVIYNEVNSIACEILRTKNINVIP 401  
QY 432 YARQWAEACFDSYMQEAKEKWIATGYLPTFEYLENGKVSSA-----HRPCALQPILTLDI 485  
Db 402 FLKKSWTDVSKAYLVEAKWYKSGHKPNLEEYMQNARISISSPTIFVHFYCVFSDQLSIQV 461  
QY 486 PFPDHILKEVDPPSKLNDLIC--IILRLRGDTRCYKADRRAGEEASISCYMKDNPGLTE 543  
Db 462 -----LETLSQHQQNVVRCSSSVFRLANDLVTSPDELARGDVCKSIQCYMSET-GASE 513  
QY 544 EDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAF-----DISRVWHHGYYRQDGY- 597  
Db 514 DKARSHVRQMTNDLWDEMNYEKMAHSSSI-----LHDFMETVINLARMSQCMYQYGDGHG 569  
QY 598 SFANVETKSLVMRTVIEPVPL 618  
Db 570 SPEKAKIVDRVMSLLFNPIPL 590

RESULT 5  
A56118  
vetispiradiene synthase 1 - Hyoscyamus muticus (fragment)  
C;Species: Hyoscyamus muticus  
C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 29-Sep-1999  
C;Accession: A56118  
R;Back, K.; Chappell, J.  
J. Biol. Chem. 270, 7375-7381, 1995

A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus mut.  
A;Reference number: A56118; MUID:95221394; PMID:7706281  
A;Accession: A56118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-520 <BAC>

A;Cross-references: GB:U20188; NID:g763422; PIDN:AAA86337.1; PID:g763423

C;Superfamily: vetispiradiene synthase 1

Query Match 20.6%; Score 669.5; DB 2; Length 520;  
Best Local Similarity 31.2%; Pred. No. 2.5e-39;  
Matches 161; Conservative 111; Mismatches 211; Indels 33; Gaps 13;

QY 112 GNDLLQRLLLVDDVERLIGDRHFKEIKTALDYV--NSYWNEKGICGGRSVVTDLNST 168  
Db 29 GTTLTEKLNLDITIERLGIAYHFKEQIEDMLDHIYRADPYF-----EAHEYNDLNTS 80  
QY 169 ALGLRTLRLHGTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGK 228  
Db 81 SVQFRLLRQHGYNVSPNIFSRFQDANGKFES----LRSDIRGLLNLYEASHVTRHKEDI 136  
QY 229 MDEAETFSTKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLARNYMDVFGQHTKNK 288  
Db 137 LEEALVFSVGHLESAAPHL--KSPLSKQVTHALEQSLHKSIPRVEIRYFISY-EEEEFK 193  
QY 289 NAAEKLLELAKLEFNIFHSLQERELKHVSRWVKD-SGSPMTFCRHRHVEYYALASCI 347  
Db 194 N--DLLRFAKLDYNLLQMLHKHELSEVSRWVKDLDFVTTLPYARDRAVECYFWTMGVYA 251  
QY 348 EPQHSGRFLGFTKMSHLITVLDDMYDVFQTVDELELFTATIKRWDPDSAMECLPEYMKGVY 407  
Db 252 EPQYSQARVMLAKTIAMISIVDDTFDAYGIVKELEVYTDAIQRWDISQIDRLPEYMKISY 311  
QY 408 MMVYHTVNMARVAEKAQGRDTLNYARQWAEACFDSYMQEAKEKWIATGYLPTFEYLENGK 467  
Db 312 KALLDLYDDYKEKLSKGRSDVVHYAKERMKEIVGNFYFIEGKWFIEGYMPSVSEYLSNAL 371  
QY 468 VSSAHRPCALQPILTLDIPFPDHILKEVDFFPSKL--NDLICILRLRGDTRCYKADRARG 525  
Db 372 ATSTYLLTTSYLGKMSATKEHFEWLATNPKILEANATLC---RVVDDIATYEVEKGRG 428  
QY 526 EEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSK--KHAFDI 583  
Db 429 QIATGIECYMRDY-GVSTEVAMEKFQEMADIWKDVNEEILRP---TPVSSSEILTRILNL 484  
QY 584 SRVWHHGYYR-RDGYSFANVETKSLVMRTVIEPVPL 618  
Db 485 ARIIDVTYKHNQDGYTHPEKVLKPHIALVVDSDI 520

RESULT 6

F71434

probable limonene cyclase - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Variety: columbia

C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 20-Jun-2000

C;Accession: F71434

R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks  
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giele  
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,  
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansc  
C.; Chalwatzis, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thali

A;Reference number: A71400; MUID:98121113; PMID:9461215

A;Accession: F71434

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-600 <BEV>

A;Cross-references: GB:Z97341; NID:g2244991; PID:g2245028

C;Genetics:

A;Map position: 4COP9-4G3845





Db	16	EEIIRPVADSFPSLWGDRLFSPSIDNQVETKYAQ-----EIEBLKEQTRSMLL	63
QY	110	DGGNDLLQRLLLVDDVERLGDIDRHFKKEIKTALDYV-NSYWNEKGIGCGRESVVTDLNST	168
Db	64	ASGRKLSSETLNLIDVIERLGIAYHFEKEIDEILDRIYNENSFEG-----DVYNEDLCTC	118
QY	169	ALGLRTLRLHGYTVSSDVNLNVFKDKNGQFSSSTANIQIEGEIRGVNLNLFASLVAFPGEKV	228
Db	119	RLQFRLLRQHGINISLKIFSKFLDGNRLKES----LASDVLGLLSLYEASHVRSHGEDI	174
QY	229	MDEAETFSTKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLRLEARNYMDVFGQHTKNK	288
Db	175	LEDALAFSTTHLESATPHLEYP--LKEQVRHALEQSLHKGIPRIEIQFFISSVYDQKAIK	232
QY	289	NAAEKLLELAKLEFNIFHSLQERELKHVSRWWKDSGSPE-MTFCRHRHVEYYALASCIAF	347
Db	233	N--DVLLRFKALDYNMLQMLHKQELAEVSRWWKDLNFVNTLTPYARDRVVECYFWALGVYY	290
QY	348	EPQHS GFRLGFTKMSHLITVLDDMYDVFVGTVDELELFTATIKRWDPSAMECLPEYMKGVY	407
Db	291	EPQYSQARVMLVKTIAMISIVDDTYDAYGTVDELAITYDVIQRWDIKEIDSLPDYMK---	347
QY	408	MMVYHTVNEMARVAEKAQGRD----TLNLYARQAWAEACFDSYMQEAKWIATGYLPTFEEYL	463
Db	348	-ISYKALLDLVYDYEKEMSRDGRSHVVVYAKERLKLKELVKSYNIEAKWFIEGHMPPASEYL	406
QY	464	ENGVSSAHRPCALQPILTLDPFPDHILKEVDFP--SKLNDLI--CI-ILRLRGDTRCY	518
Db	407	RNAFVTTTTYYLATTSYLG-----KYAKEQPEWLKSNPKILEGCVTICRVIDDYATY	460
QY	519	KADRARGEAEASSICYMKDNPGLTEEDALNHNFMIRDARELNWELLKXPNVSPITSKK	578
Db	461	EVEKNRGQLSTGIECYMRDYSVSTKE-AMAKFQEMGESGWKDINEGMRLP-TPIPMEFLS	518
QY	579	HAFDISRVVHHGYRY-RDGYSFANVETKSLVMRTVIE	614
Db	519	RILNLARLVDTYIKHNEDGYTHPEKVIKPHIIAMVVD	555
RESULT 9			
T06266			
germacrene C synthase - tomato			
C;Species: Lycopersicon esculentum (tomato)			
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000			
C;Accession: T06266			
R;Colby, S.M.; Crock, J.; Dowdle-Rizzo, B.; Lemaux, P.G.; Croteau, R.			
Proc. Natl. Acad. Sci. U.S.A. 95, 2216-2221, 1998			
A;Title: Germacrene C synthase from Lycopersicon esculentum cv. VFNT Cherry tomato: cDNA			
A;Reference number: Z15576; MUID:98151492; PMID:9482865			
A;Accession: T06266			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-548 <COL>			
A;Cross-references: EMBL:AF035631; NID:g2967688; PIDN:AAC39432.1; PID:g2967689			
A;Experimental source: cultivar VFNT			
C;Superfamily: vetispiradiene synthase 1			
Query Match 18.9%; Score 615.5; DB 2; Length 548;			
Best Local Similarity 27.0%; Pred. No. 1.7e-35;			
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QY	52	ASTDSVQRRVGNVHSLWDDDFI-----QSLISTPYGAPDYRERADRLIGEVDIMF	103
Db	3	ASSADKCRPLANFHPSPVWGYPHFLSYTHEITNQEKVE----VDEYKETIRKMLVETCD---	55
QY	104	NFKSLEDGGNDLLQRLLLVDDVERLGDIDRHFKKEIKTALDYV--NSYWNEKGIGCGRES	160
Db	56	-----NSTQKLVLIDAMQRLGVAYHFDNEIETSIQNI F DASSKQNDND-----	98
QY	161	VVTDLNSTALGLRTLRLHGYTVSSDVNLNVFKDKNGQFSSSTANIQIEGEIRGVNLNLFASL	220
Db	99	--NNLYVVSRLRFLRVQQGHYMSDDVFKQFTNQDGKFKE-----LTNDVQGLLSLYEASH	152
QY	221	VAFPGEKVMDEAETFSTKYLREALQKIP-ASSILSLEIRDVLEYGWHTNLPRLRLEARNYMD	279
Db	153	LRVRNEEILEEALTFTTHLESIVSNLSNNNSLKVEVGEALTQPIRMTLPRMGARKYIS	212
QY	280	VFGQHTKNKNAEK-LLELAKLEFNIFHSLQERELKHVSRWWKDSGSPEMTFCRHRHVE	337
Db	213	IY----ENNDAHHHLLLKFAKLDNFMLQKHQRELSDLTRWWKOLDFANKYPYARDRLVE	268
QY	338	YYALASCIAFEPOHSGFRLGFTKMSHLITVLDDMYDVFVGTVDELELFTATIKRWDPSAME	397

QY	221	VAFPGEKVMDEAETFSTKYLREALQKIP-ASSILSLEIRDVLEYGWHTNLPRLRLEARNYMD	279
Db	153	LRVRNEEILEEALTFTTHLESIVSNLSNNNSLKVEVGEALTQPIRMTLPRMGARKYIS	212
QY	280	VFGQHTKNKNAEK-LLELAKLEFNIFHSLQERELKHVSRWWKDSGSPEMTFCRHRHVE	337
Db	213	IY----ENNDAHHHLLLKFAKLDNFMLQKHQRELSDLTRWWKOLDFANKYPYARDRLVE	268
QY	338	YYALASCIAFEPOHSGFRLGFTKMSHLITVLDDMYDVFVGTVDELELFTATIKRWDPSAME	397
Db	269	CYFWILGVYFEPKYSRARKMTTKVLNLTISIDDTDFDAYATFDELVTENDAIQRWDANAID	328
QY	398	CLPEYMKGVMMVYHTVNEMARVAEKAQGRDTLNYARQAWAEACFDSYMQEAKWI-ATGYL	456
Db	329	SIQYMRPAYQALLDIYSEMEQVLSKEGLDRVYAKNEMKKLVRAYFKETQWLNDCDHI	388
QY	457	PTFEEYLENGKVSSAHRPCALQPILTLDPFPDHILKEVDFPSPKLNLDLI-----CIILRL	511
Db	389	PXYEEQVENAIVSAGY----MMISTTCLVGIEEFISHETFEWLMNESVIVRASALIARA	443
QY	512	RGDTRCYKADRARGEAEASSICYMKDNPGLTEEDALNHNFM--IRDATRELNWELLKPD	569
Db	444	MNDIVGHEDEQERGHVASLIECYMKDYGASKQE---TYIKFLKEVTNAWKDINKQFSRP-	499
QY	570	NSVPITSKKHAFDISRVVHHGYRYRDGYSFANVETKSLVMRTVIEPVPL	618
Db	500	TEVPMFVLERVLNLTRVADTLYKEKDTYSTAKGKLKNMINPILIESVKI	548
RESULT 10			
T06265			
germacrene C synthase, epidermal - tomato			
C;Species: Lycopersicon esculentum (tomato)			
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000			
C;Accession: T06265			
R;Colby, S.M.; Crock, J.; Dowdle-Rizzo, B.; Lemaux, P.G.; Croteau, R.			
Proc. Natl. Acad. Sci. U.S.A. 95, 2216-2221, 1998			
A;Title: Germacrene C synthase from Lycopersicon esculentum cv. VFNT Cherry tomato: cDNA			
A;Reference number: Z15576; MUID:98151492; PMID:9482865			
A;Accession: T06265			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-548 <COL>			
A;Cross-references: EMBL:AF035630; NID:g2967686; PIDN:AAC39431.1; PID:g2967687			
A;Experimental source: cultivar VFNT			
C;Superfamily: vetispiradiene synthase 1			
Query Match 18.9%; Score 614.5; DB 2; Length 548;			
Best Local Similarity 26.8%; Pred. No. 2e-35;			
Matches 158; Conservative 137; Mismatches 229; Indels 65; Gaps 16;			
QY	52	ASTDSVQRRVGNVHSLWDDDFI-----QSLISTPYGAPDYRERADRLIGEVDIMF	103
Db	3	ASSADKCRPLANFHPSPVWGYPHFLSYTHEITNQEKVE---VDEYKETIRKMLVETCD---	55
QY	104	NFKSLEDGGNDLLQRLLLVDDVERLGDIDRHFKKEIKTALDYV--NSYWNEKGIGCGRES	160
Db	56	-----NSTQKLVLIDAMQRLGVAYHFDNEIETSIQNI F DASSKQNDND-----	98
QY	161	VVTDLNSTALGLRTLRLHGYTVSSDVNLNVFKDKNGQFSSSTANIQIEGEIRGVNLNLFASL	220
Db	99	--NNLYVVSRLRFLRVQQGHYMSDDVFKQFTNQDGKFKE-----LTNDVQGLLSLYEASH	152
QY	221	VAFPGEKVMDEAETFSTKYLREALQKIP-ASSILSLEIRDVLEYGWHTNLPRLRLEARNYMD	279
Db	153	LRVRNEEILEEALTFTTHLESIVSNLSNNNSLKVEVGEALTQPIRMTLPRMGARKYIS	212
QY	280	VFGQHTKNKNAEK-LLELAKLEFNIFHSLQERELKHVSRWWKDSGSPEMTFCRHRHVE	337
Db	213	IY----ENNDAHHHLLLKFAKLDNFMLQKHQRELSDLTRWWKOLDFANKYPYARDRLVE	268
QY	338	YYALASCIAFEPOHSGFRLGFTKMSHLITVLDDMYDVFVGTVDELELFTATIKRWDPSAME	397

Db	269	CYFWILGVYFEPKYSRARKMMTKVNLNLTISIDDTFDAYATFDELVTFNDAIQRDANAID	328
QY	398	CLPEYMKGVNMYHTVNEMARVAEKAQGRDFTLNYARQAWAEACFDSYMQEAKWI-ATGYL	456
Db	329	SIQPYMRPAYQALLDIYSEMEQVLSKEGKLDRVVYAKNEMKKLVRAYPEKETQWLNCDDHI	388
QY	457	PTFEEYLENGKVSSAHRPCALQPILTLTDIPFPDHILKEVDFFPSKLNDLI-----CIILRL	511
Db	389	PKYEEQVENAIVSAGY-----MMISTTCLVGIIEEFISHETFELWMNESVIVRASALIARA	443
QY	512	RGDTRCYKADRARGEAEASSISCYMKDNPGLTTEDALNHINFM--IRDARELNWELLKPD	569
Db	444	MNDIVGHEDEQERGHVASLIECYMKDYGASKQE---TYIKELKEVTNAWKDINKQFERP-	499
QY	570	NSVPITSKKHAFDISRVVHHGYRYRDGYSPANVETKSLVMRTVIEPVPL	618
Db	500	TEVPMFVLERVNLTRVADTLYKEKDTYTNAGKGLKMNINSILIESVKI	548
RESULT 11			
G71434			
probable limonene cyclase - Arabidopsis thaliana			
C;Species: Arabidopsis thaliana (mouse-ear cross)			
A;Variety: columbia			
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998			
C;Accession: G71434			
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk			
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel			
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.			
Nature 391, 485-488, 1998			
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech			
erhof, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans			
C.; Chalwatzis, N.			
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal			
A;Reference number: A71400; MUID:98121113; PMID:9461215			
A;Accession: G71434			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-1024 <BEV>			
A;Cross-references: GB:Z97341; NID:g2244991; PID:e327011; PID:g2245029			
C;Genetics:			
A;Map position: 4COP9-4G3845			
Query Match 18.0%; Score 586.5; DB 2; Length 1024;			
Best Local Similarity 30.2%; Pred. No. 4.8e-33;			
Matches 163; Conservative 109; Mismatches 195; Indels 73; Gaps 17;			
QY	86	DYRERADRLIGEVDIMFNFKSLEDGGNDLLQRLLLVDDVERLGIDRHFHFKKEIKTALDYV	145
Db	5	DNVERVTLKQEVSKML-----NETEGLLEQLELIDTLQRLGVSYHFEQEIKKTLTNV	57
QY	146	NSYWNEKGIGCGRESVVT---DLNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTA	201
Db	58	-----HVKNVRAHKNRIDRNRWGDLYATALEFRLLRQH-----DV-----FDGNI	97
QY	202	NIQIEG-EIRGVNLFRASLVAFPGEKVMDEAETFTSKYLR---EALQKIPASSILSLEI	257
Db	98	GVDLDDKDIKGILSLYBASYLSTRIDTKLKESTYVTTKRLRFVEVKNKNETKSYTLRRMV	157
QY	258	RDVLEYGHTNLPRLERNYMDVFGQ-HTKNKNAAEKLELAKLEFNIFHSIQERELKHV	316
Db	158	IHALEMPYHRRVGRLEARWYIEVYGERHDMN----PILLELAKLDENFVQATHQDELKSL	213
QY	317	SRWKDSG-SPEMTFCRRHRYEYYALASCIAPFQHSGRFLGFTKMSHLITVLDDMYDVF	375
Db	214	SSWWSKTGLTKHLDFVDRITEGYFSSVGVMYEPFAYHRQMLTKVFMLLITIDDIYDIY	273
QY	376	GTVDELELFTATIKRWDPSAMECLPEYMKGVNMYHTVNEMARVAEKAQGRDTLNYARQ	435
Db	274	GTLEELQLFTTIVEKWDVNRLEELPNYMKLCFLCLVNEINQIGYFVLKRGFNVIPYLKE	333
QY	436	AWAEACFDSYMQEAKWIATGYLPTFEEYLENGKVSSA-----HRPCALQPILTLDI--PF	487

Db	334	SWADMCTTFLKEAKWKYSGYKPNFEEYMQNGWISSSVPTILLHLFCLLSD-QTLDILGSY	392
QY	488	PDHILKEVDFPSKLNLDLICIILRLRGD-----TRCYKADRARGEAEASSISCYMKD	537
Db	393	NHSVVR-----SATILRLANDLATSSVSHGFTTYNTEELARGDTMKSVQCHMHE	442
QY	538	NPGLTEEDALNHINFMIRDARELNWELLKPDNSVPITSKGHAFDISRVVHHGYRYRDGY	597
Db	443	T-GASEAESRAYIQGIIGVAWDDLNME--KKSCRLHQGFLEAAANLGRVAQCYYQYGDGH	499
RESULT 12			
E96723			
hypothetical protein F20P5.19 [imported] - Arabidopsis thaliana			
C;Species: Arabidopsis thaliana (mouse-ear cross)			
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001			
C;Accession: E96723			
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,			
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,			
ansen, N.F.; Hughes, B.; Huizar, L.			
Nature 408, 816-820, 2000			
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C			
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,			
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.			
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,			
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.			
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.			
A;Reference number: A86141; MUID:21016719; PMID:11130712			
A;Accession: E96723			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-632 <STO>			
A;Cross-references: GB:AE005173; NID:g2194130; PIDN:AAB61105.1; GSPDB:GN00141			
C;Genetics:			
A;Gene: F20P5.19			
A;Map position: 1			
C;Superfamily: vetispiradiene synthase 1			
Query Match 17.5%; Score 569; DB 2; Length 632;			
Best Local Similarity 26.5%; Pred. No. 4e-32;			
Matches 174; Conservative 120; Mismatches 276; Indels 86; Gaps 18;			
QY	10	VSRSC---LSSSHEIKALRRTIPTLGICRPGKSVAHSNMCL----TSVASTDSVQRRV	61
Db	16	LSRLCWRLNLSSYHYPLLKSSLSFSRFQSPKK-----LCLVRATTNPTDDNSTTRSF	68
QY	62	GNYHSNLWDDDFIQSLISTPYGAPDYRERAD--RLIGEVDIMFNFKSLEDGGNDLLQRL	119
Db	69	TPHPPSLWGHFELSASV-----NQTEMDDLWRQIEALKPIV-NAMLLPCNGADAKKIT	120
QY	120	LLVDDVERLGIDRHFHFKKEIKTALDYVNSYWNEKGIGCGRESVVTDLNSTALGLRTLRLHG	179
Db	121	CFIHTLVSLGVSYHFEKIVEFLKDAFENIEDMIIDCKED---DLTYVTSIFRVFRLYG	176
QY	180	YTVSS-----DVLNVFKDKNGQFSSTANIQIEGEIRGVNLNLFRA	218
Db	177	HYITPELHITISYVFFFLIFHTCMCVDFINRPFKGGDGNFKKCLN----DDVRGMLSFYEA	232
QY	219	SLVAFPGKEKVMDEAETFTSKYLREAL--QKIPASSILSLEIRDVLVLEYGWHHTNLPRLERN	276
Db	233	SHFGTTEDILBEAMSFTQKHLEFLVGEKAKHYPHITKLIQAALYIPQNFNLEILLVARE	292
QY	277	YMDVFGQHTKNKNAAEKLELAKLEFNIFHSLOERELKHVSRWK--DSGSPEMTFCRHR	334
Db	293	YIDFYELETDHN---EMLLKLAKLNRFRFLQYIQDLTKLTLTWWKELDLVSKIPVYFRER	349
QY	335	HVEYYALASCIAPFQHSGRFLGFTKMSHLITVLDDMYDVGFTVDELELFTATIKRWDPS	394
Db	350	LAEPYFWATGIYEPQYSAARIMLAKSIILVDIVDNTFDVYGTIDEVKSLLVQAIERWDS	409
QY	395	AMECLPEYMKGVNMYHTVNEMARVAEKAQGRDTLNYARQAWAEACFDSYMQEAKWIATG	454
Db	410	AVDVLPDYLVKVVVFTFDLFKELEEYVSSEARSFTMQAYEQLEQLRILMKGYLQEAESNRG	469







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:38:32 ; Search time 17 Seconds  
(without alignments)  
1892.903 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRSLSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2453	75.5	628	1	TSD1_ABIGR	O24475 abies grand
2	2200.5	67.7	627	1	TSD2_ABIGR	O24474 abies grand
3	2031.5	62.5	637	1	TSD3_ABIGR	O22340 abies grand
4	1240.5	38.2	862	1	TASY_TAXBR	Q41594 taxus brevi
5	1238.5	38.1	862	1	TASY_TAXBA	Q93va3 taxus bacca
6	1209.5	37.2	862	1	TASY_TAXCH	Q9ft37 taxus chine
7	717.5	22.1	554	1	DCS1_GOSAR	Q39761 gossypium a
8	717.5	22.1	554	1	DCS2_GOSAR	Q39760 gossypium a
9	701.5	21.6	554	1	DCS4_GOSAR	O49853 gossypium a
10	699.5	21.5	555	1	DCS3_GOSAR	Q43714 gossypium a
11	692.5	21.3	554	1	DCS1_GOSHI	P93665 gossypium h
12	667	20.5	601	1	CASS_RICCO	P59287 ricinus com
13	644.5	19.8	548	1	SEAS_TOBAC	Q40577 nicotiana t
14	133	4.1	1941	1	UBR1_KLULA	O60014 kluuveromyc
15	125	3.8	1295	1	BXA2_CLOBO	Q45894 clostridium
16	117.5	3.6	1513	1	GRLF_RAT	P81128 rattus norv
17	114	3.5	456	1	PUR8_ECOLI	P25739 escherichia
18	111.5	3.4	602	1	LEPA_HELPY	O25122 helicobacte
19	110	3.4	2875	1	RRPL_TSWV1	P28976 tomato spot
20	109.5	3.4	1513	1	GRLF_HUMAN	Q9nry4 homo sapien
21	108.5	3.3	570	1	EZRA_BACAA	Q81xt8 bacillus an
22	108.5	3.3	1061	1	EX5C_BUCAP	Q8k9b0 buchnera ap
23	107	3.3	815	1	CC53_YEAST	Q12018 saccharomyc
24	105.5	3.2	428	1	SYS_FASMU	P57836 pasteurella
25	105.5	3.2	898	1	YMV6_YEAST	Q04748 saccharomyc
26	105.5	3.2	1026	1	MY1B_DROME	Q23979 drosophila
27	105	3.2	1790	1	VIT_ANTGR	Q05808 anthonomus
28	104.5	3.2	510	1	CHLB_PINTH	Q00864 pinus thunb
29	104.5	3.2	570	1	EZRA_BACCR	Q817a9 bacillus ce
30	104.5	3.2	1500	1	GRLF_CANFA	P83509 canis famil
31	104	3.2	1510	1	MUKB_HAEIN	P45187 haemophilus
32	103.5	3.2	598	1	SYD_LACPL	Q88vg8 lactobacill
33	103.5	3.2	822	1	V2A_BMV	P03594 brome mosai

RESULT 1						
TSD1_ABIGR						
ID	TSD1_ABIGR	STANDARD;	PRT;	628 AA.		
AC	O24475;					
DT	28-FEB-2003 (Rel. 41, Created)					
DT	28-FEB-2003 (Rel. 41, Last sequence update)					
DT	10-OCT-2003 (Rel. 42, Last annotation update)					
DE	Pinene synthase, chloroplast precursor (EC 4.2.3.14) (Beta-geraniolene synthase) ((-)-(1S,5S)-pinene synthase).					
GN	AG3.18.					
OS	Abies grandis (Grand fir).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.					
OX	NCBI_TaxID=46611;					
RN	[1]					
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.					
RX	MEDLINE=97413772; PubMed=9268308;					
RA	Bohlmann J., Steele C.L., Croteau R.;					
RT	"Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";					
RT	J. Biol. Chem. 272:21784-21792(1997).					
CC	-!- FUNCTION: Involved in defensive oleoresin formation in conifers in response to insect attack or other injury. Involved in monoterpene (C10) olefins biosynthesis. A mixture of alpha-and beta-pinene is produced by this enzyme.					
CC	-!- CATALYTIC ACTIVITY: Geranyl diphosphate = pinene + diphosphate.					
CC	-!- COFACTOR: Manganese and potassium.					
CC	-!- PATHWAY: Oleoresinosis.					
CC	-!- SUBCELLULAR LOCATION: Chloroplast.					
CC	-!- INDUCTION: By wounding.					
CC	-!- SIMILARITY: Belongs to the terpene synthase family.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC	EMBL; U87909; AAB71085.1; -.					
CC	HSSP; Q40577; SEAT.					
DR	InterPro; IPR008930; Terp_cyc_toroid.					
DR	InterPro; IPR001906; Terp_synth-like.					
DR	InterPro; IPR005630; Terpene synth C.					
DR	InterPro; IPR008949; Terpenoid_synth.					
DR	Pfam; PF01397; Terpene_synth; 1.					
DR	Pfam; PF03936; Terpene_synth_C; 1.					
KW	Lyase; Manganese; Transit peptide; Chloroplast.					
FT	TRANSIT 1 ? CHLOROPLAST (POTENTIAL).					
FT	CHAIN ? 628 PINENE SYNTHASE.					
FT	ACT_SITE 524 524 BY SIMILARITY.					
FT	ACT_SITE 601 601 BY SIMILARITY.					
FT	ACT_SITE 605 605 BY SIMILARITY.					
SEQUENCE	628 AA; 71505 MW; 23DBB78BF3C8072C CRC64;					

ALIGNMENTS











Db 519 DDDYVWQRKTLRMPSLNSKCLELAKLDENIVQSLHQEELKLLTRWWKESGMADINFTR 578  
QY 333 HRHVEYYALASCIAPFQHSGLRFTKMSHLITVLDMDYDFVGTVDLELFTATIKRWD 392  
Db 579 HRVAEVY--FSSATFEPEYSATRIAFKIGLQVLFDMDADIFATLDELKSFTEGVKRW 636  
QY 393 PSAMECLPEYMKGVMMVYHTVNEMARVAEKAQGRDTLNYARQAWAEACFDSYMQAEKWIA 452  
Db 637 TSLLHEIPECMQTCFKVWFKLMEEVNNDVVKQGRDMLAHIRKPWELYNFCYVQEREWLE 696  
QY 453 TGYLPTFEEYLENGKVSSAHRPCALQPILTLDIPFPDHILKEVDFPKSLNDLICIILRLR 512  
Db 697 AGYIPTFEEYLYKTYAISVGLGPCTLQPILLMGELVKDDVVEKVHYPSPNFELVLSWRLT 756  
QY 513 GDTRCYKADRARGEAEASSISCYMKONPGLTEEDALNHINFIMIRDAIRELNWELLKPDNSV 572  
Db 757 NDTKTYQAEKARQQQASGIACYMKONPGATEEDAIAKHICRVVDRLAKEASFEYFKPSNDI 816  
QY 573 PITSKKHAFDISRVVWHHGYYRDRDGYSFANVETKSLVMRTVIEPV 616  
Db 817 PMGCKSFIFNLRLCVQIFYKFIDGYGIANEEIKDYIRKVYIDPI 860

RESULT 6  
TASY TAXCH STANDARD; PRT; 862 AA.  
AC Q9FT37;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene synthase).  
GN TDC1.  
OS Taxus chinensis (Chinese yew).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.  
OX NCBI\_TaxID=29808;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Callus;  
RA Wang W., Shi Q., Ouyang T., Zhu P., Cheng K.;  
RT "Cloning, expression, and characterization of taxadiene synthase, a  
diterpene cyclase from Taxus chinensis."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid  
intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the  
parent olefin with a taxane skeleton.  
CC -!- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene +  
diphosphate.  
CC -!- PATHWAY: Taxol biosynthesis; first step.  
CC -!- SIMILARITY: Belongs to the terpene synthase family.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AY007207; AAG02257.1; --.  
DR HSP; Q40577; SEAU.  
DR InterPro; IPR008930; Terp\_cyc\_toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR InterPro; IPR005630; Terpene\_synth\_C.  
DR InterPro; IPR008949; Terpenoid\_synth.  
DR Pfam; PF01397; Terpene\_synth; 1.  
DR Pfam; PF03936; Terpene\_synth; 1.  
KW Taxol biosynthesis; Lyase.  
FT ACT\_SITE 758 BY SIMILARITY.  
FT ACT\_SITE 835 BY SIMILARITY.  
FT ACT\_SITE 839 BY SIMILARITY.  
SQ SEQUENCE 862 AA; 98069 MW; 3A597BAF722BF679 CRC64;

Query Match 37.2%; Score 1209.5; DB 1; Length 862;  
Best Local Similarity 41.9%; Pred. No. 4.9e-74;  
Matches 270; Conservative 110; Mismatches 209; Indels 55; Gaps 12;  
QY 15 LSSSHEI--KALRRTIPTLIGICRPG-----KSAHSINMCLTSV-ASTDSVQRRVGNYS 66  
Db 230 LSPDFEIIFFALLQKAKALGINLPYDLPEIKYLSSTREARLTVDVSAADNIPANMLNALE 289  
QY 67 NL-----W-----DDDFIQSLISTPYGAPDYRERADRLLIGEVDIMFNFKS---LE 109  
Db 290 GLEEVMDWKIMRFQSKDGSFLSSPAST-----ACVLMNTGDEKCFTEFLNNLLVK 339  
QY 110 DGG-----NDLLQRLLLVDDVERLGDIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVV 162  
Db 340 FGGCVPCMYSIDLLERLSLVDNIEHLGIGRHFKEIKVALDYVYRHSERGIWGRDSL 399  
QY 163 TDLNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQPSSTANIQIEGEIRGVNLFRASLVA 222  
Db 400 PDLNTTALGLRTLRTHTGYDVSSDVLNFKDENGRRFFSSAG-QTHVELRSVVILFRASDLA 458  
QY 223 FPGEKVMDEAETFTSKYLREAL-QKIPASSILSLEIRDVLEYGWHHTNLPRLEARNYMDVF 281  
Db 459 FPDEGAMDDARKFAEPYLRDALATKISTNTKLFKEIEYVVEYPWHMSIPRSEARSYIDS 518  
QY 282 GQ-----HTKNKNAAEKLELAKLEFNIFHSLQERELKHVSRWVKDGSPEMTFCR 332  
Db 519 DDDYVWERKTLRMPSLNSKCLELAKLDENIVQSLHQEELKLLTRWWKESGMADINFTR 578  
QY 333 HRHVEYYALASCIAPFQHSGLRFTKMSHLITVLDMDYDFVGTVDLELFTATIKRWD 392  
Db 579 HRVAEVY--FSSATFEPEYSATRIAFKIGLQVLFDMDADIFATLDELKSFTEGVKRW 636  
QY 393 PSAMECLPEYMKGVMMVYHTVNEMARVAEKAQGRDTLNYARQAWAEACFDSYMQAEKWIA 452  
Db 637 TSLLHEIPECMQTCFKVWFKLIIEVNNDVVKQGRDMLAHIRKPWELYNFCYVQEREWLD 696  
QY 453 TGYLPTFEEYLENGKVSSAHRPCALQPILTLDIPFPDHILKEVDFPKSLNDLICIILRLR 512  
Db 697 AGYIPTFEEYLYKTYAISVGLGPCTLQPILLMGELVKDDVVEKVHYPSPNFELVLSWRLT 756  
QY 513 GDTRCYKADRARGEAEASSISCYMKONPGLTEEDALNHINFIMIRDAIRELNWELLKPDNSV 572  
Db 757 NDTKTYQAEKARQQQASGIACYMKONLGAATEEDAIAKHICRVVDRLAKEASFEYFKPSNDI 816  
QY 573 PITSKKHAFDISRVVWHHGYYRDRDGYSFANVETKSLVMRTVIEPV 616  
Db 817 PMGCKSFIFNLRLCVQIFYKFIDGYGIANEEIKDYIRKVYIDPI 860  
RESULT 7  
DCS1\_GOSAR STANDARD; PRT; 554 AA.  
ID DCS1\_GOSAR  
AC Q39761;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE (+)-delta-cadinene synthase isozyme XCl (EC 4.2.3.13) (D-cadinene  
synthase).  
DE Gossypium arboreum (Tree cotton).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
OX NCBI\_TaxID=29729;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nanking;  
RX MEDLINE=96132653; PubMed=8554317;  
RA Chen X.-Y., Chen Y., Heinstein P., Davisson V.J.;  
RT "Cloning, expression, and characterization of (+)-delta-cadinene  
synthase: a catalyst for cotton phytoalexin biosynthesis."  
RL Arch. Biochem. Biophys. 324:255-266(1995).  
CC -!- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl  
diphosphate (FPP) to (+)-delta cadinene.

CC -!- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-  
CC delta-cadinene + diphosphate.  
CC -!- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;  
CC first (committed) step.  
CC -!- SIMILARITY: Belongs to the terpene synthase family.  
CC -----  
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CC -----  
DR EMBL; U23206; AAA93064.1; -.  
DR PIR; S68365; S68365.  
DR HSSP; Q40577; SEAU.  
DR InterPro; IPR008930; Terp\_cyc toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR InterPro; IPR005630; Terpene\_synth\_C.  
DR InterPro; IPR008949; Terpenoid\_synth.  
DR Pfam; PF01397; Terpene\_synth\_1.  
DR Pfam; PF03936; Terpene\_synth\_C; 1.  
KW Lyase; Multigene family.  
FT ACT\_SITE 451 BY SIMILARITY.  
FT ACT\_SITE 527 BY SIMILARITY.  
FT ACT\_SITE 531 BY SIMILARITY.  
SQ SEQUENCE 554 AA; 64137 MW; 59D6922DED9DCAF CRC64;  
  
Query Match 22.1%; Score 717.5; DB 1; Length 554;  
Best Local Similarity 31.8%; Pred. No. 4.7e-41;  
Matches 183; Conservative 107; Mismatches 243; Indels 43; Gaps 14;  
  
QY 51 VASTDSVQRRVGNVHNSNLWDDDFIQSLISTPYGAPD-----YRERADRLIGEVDIMFN 104  
Db 14 LSSNKMDEMRPKADFPQPSIWGDLFL-----NCPDKNIDAETERHQQLKEVR----- 60  
  
QY 105 FKSLEDGGNDLLQRLLLVDDVERLIGDRHFKEIKTALDYVNSYWNKEGICGGRSVVTD 164  
Db 61 -KMIVAPMANSTQKLAFIDSVQRLGVSYHFTKEIDELE--NIYHN-----NDAEND 110  
  
QY 165 LNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFP 224  
Db 111 LYTTTSIRFRLRLRHGYNVSCDVFNKFKDEQGNFKSS----VTSDVRGLLELYQASYLRVH 166  
  
QY 225 GEKVMDEAETFTSKYLREALQKIPASSILSLRIDVLEYGWHTNLPRLRNMDVFGQH 284  
Db 167 GEDILDEAISTFTHHLSLAVASL--DHPLSEEVSHALKQSIRRGRLPRVEARHYSVY-QD 223  
  
QY 285 TKNKNAAEKLEELAKLEFNIFHSLQERLKHVSRWWD-SGSPMTFCRRHRHVEYYALAS 343  
Db 224 IESHNKA--LLEFAKIDFNMLQFLHRKELSEICRWKKDLDFQRKLPYARDRVVEGYFWIS 281  
  
QY 344 CIAFEPQHSGRFLGFTKMSHLITVLDDMYDVGTVDELELFTATIKRWDPSSAMECLPEYM 403  
Db 282 GVFEPQYSLGRKMLTKVIAMASIVDDTYDSYATYEEELIPYTNAIERWDIKCIDEIPEYM 341  
  
QY 404 KGVYMMVYHTVNEMARVAEKAQGRDTLNVARQAEACFDSYMQEAKWIATGYLPTFEEYL 463  
Db 342 KPSYKALLDVVEEMVQLVAEHGRQYRVEYAKNAMIRLAQSYLVEAKWTQLQNYKPSFEFK 401  
  
QY 464 ENGVSSAHRPCALQPIITL-DIPFPDHILKEVDFPFSKLNLDLICIILRLGDTRCYKADR 522  
Db 402 ANALPTCGYAMLATISFVGMDIVTPTETFKWAASDP-KIIQASTIICRFMDDDVAEHKFKH 460  
  
QY 523 ARGEAASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKAFD 582  
Db 461 RREDDCSAIECYMEEV-GVTAQEAAYDVFNKHVESAWKDLNQEFKLP-TEMPTEVLNRSLN 518  
  
QY 583 ISRVVHHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618  
Db 519 LARVMDVLYREGDGYTVVGKAAKGGITSLLEIPAL 554

RESULT 8

DCS2\_GOSAR STANDARD; PRT; 554 AA.  
AC Q39760;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE (+)-delta-cadinene synthase isozyme XC14 (EC 4.2.3.13) (D-cadinene  
DE synthase).  
OS Gossypium arboreum (Tree cotton).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
OX NCBI\_TaxID=29729;  
RN [1]\_SEQUENCE FROM N.A.  
RC STRAIN=cv. Nanking;  
RX MEDLINE=96132653; PubMed=8554317;  
RA Chen X.-Y., Chen Y., Heinsteins P., Davisson V.J.;  
RT "Cloning, expression, and characterization of (+)-delta-cadinene  
RT synthase: a catalyst for cotton phytoalexin biosynthesis.";  
RL Arch. Biochem. Biophys. 324:255-266(1995).  
CC -!- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl  
CC diphosphate (FPP) to (+)-delta cadinene.  
CC -!- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-  
CC delta-cadinene + diphosphate.  
CC -!- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;  
CC first (committed) step.  
CC -!- SIMILARITY: Belongs to the terpene synthase family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U23205; AAA93065.1; -.  
DR PIR; S68366; S68366.  
DR HSSP; Q40577; SEAU.  
DR InterPro; IPR008930; Terp\_cyc toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR InterPro; IPR005630; Terpene\_synth\_C.  
DR InterPro; IPR008949; Terpenoid\_synth.  
DR Pfam; PF01397; Terpene\_synth\_1.  
DR Pfam; PF03936; Terpene\_synth\_C; 1.  
KW Lyase; Multigene family.  
FT ACT\_SITE 451 BY SIMILARITY.  
FT ACT\_SITE 527 BY SIMILARITY.  
FT ACT\_SITE 531 BY SIMILARITY.  
SQ SEQUENCE 554 AA; 64158 MW; A8897465E0F6B2B CRC64;  
  
Query Match 22.1%; Score 717.5; DB 1; Length 554;  
Best Local Similarity 31.9%; Pred. No. 4.7e-41;  
Matches 184; Conservative 108; Mismatches 241; Indels 43; Gaps 14;  
  
QY 51 VASTDSVQRRVGNVHNSNLWDDDFIQSLISTPYGAPD-----YRERADRLIGEVDIMFN 104  
Db 14 LSSNKMDEMRPKADFPQPSIWGDLFL-----NCPDKNIDAETERHQQLKEVR----- 60  
  
QY 105 FKSLEDGGNDLLQRLLLVDDVERLIGDRHFKEIKTALDYVNSYWNKEGICGGRSVVTD 164  
Db 61 -KMIVAPMANSTQKLAFIDSVQRLGVSYHFTKEIDELE--NIYHN-----NDAEND 110  
  
QY 165 LNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFP 224  
Db 111 LYTTSLRFRLLRHGYNVSCDVFNKFKDEQGNFKSS----VTSDVRGLLELYQASYLRVH 166  
  
QY 225 GEKVMDEAETFTSKYLREALQKIPASSILSLRIDVLEYGWHTNLPRLRNMDVFGQH 284  
Db 167 GEDILDEAISTFTHHLSLAVASLDP--LSEEVSHALKQSIRRGRLPRVEARHYSVY-QD 223









b	111	LYTSLRFRLLREHGFHVSCDVFNKFKDEQGNFKSS-----VTSDVRGLLELYQASYLRVH	166
y	225	GEKVMDEAETFSTKYLRREALQKIPASSILSLEIRDVLEYGWHTNLPRLRARNYMDVFGQH	284
b	167	GEDILDEAISFTSNHLSLAVASL--DHPLSEEVSHALKQSIRRGRLPRVEARHLSVY-QD	223
y	285	TKNKNAAEKLELAKLEFNIFHSLQERELKHVSRWVKD-SGSPEMTFCRHRHVEYYALAS	343
b	224	IESHN--KVLLEFAKIDFNMVQLLHRKELSEISRWVKDLDLDFQRKLPYARDRVVEGYFWIS	281
y	344	CIAFEPQHSGRFLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSSAMECLPEYM	403
b	282	GVYFEPQYSLGRKMLTKVIAMASIVDDTYDSYATYEEELIPYTNAIERWDIKCIDELPEYM	341
y	404	KGVYMMVYHTVNEMARVAEKAQGRDITLNYARQAWAEACFDSYMQAEAKWIATGYLPTFEEYL	463
b	342	KPSYKALLDVYEEMEQLVAEHGRQYRVEYAKNAMIRLAQSYLVEARWTLQNYKPSFEFEK	401
y	464	ENGVSSAHRPCALQPILTL-DIPFPDHILKEVDFPSKNDLICIILRLRGDTRCYKADR	522
b	402	ANALPTCGYAMLAIITSFVGMGDIVTPETPKWAANDP-KIIQASTIICRFMDDVTEHKFKH	460
y	523	ARGEAEASSICYMKDNPGLTEEDALNHINFIMIRDAIRELNWELLKPDNSVPITSKKHAFD	582
b	461	RREDDCSAIECYMEEY-GVTAQEAYDVFNKHVESAWKDVNQGFELKP-TEMPTTEVLNRSIN	518
y	583	ISRVWHHGYRYRDGYSFANVETKSLVMRTVIEPVPL	618
b	519	LARVMDVLYREGDGYTYVGKAAKGITSLTLLIEPIAL	554
RESULT 12			
CASS_RICCO			
ID	CASS_RICCO	STANDARD;	PRT; 601 AA.
AC	P59287;		
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Casbene synthase, chloroplast precursor (EC 4.2.3.8).		
OS	Ricinus communis (Castor bean).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae;		
OC	Ricinus.		
OX	NCBI_TaxID=3988;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94359958; PubMed=8078910;		
RA	Mau C.J., West C.A.;		
RT	"Cloning of casbene synthase cDNA: evidence for conserved structural		
RT	features among terpenoid cyclases in plants.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 91:8497-8501(1994).		
RN	[2]		
RP	CHARACTERIZATION.		
RX	MEDLINE=97115639; PubMed=8954576;		
RA	Hill A.M., Cane D.E., Mau C.J., West C.A.;		
RT	"High level expression of Ricinus communis casbene synthase in		
RT	Escherichia coli and characterization of the recombinant enzyme.";		
RL	Arch. Biochem. Biophys. 336:283-289(1996).		
CC	-!- FUNCTION: Catalyzes the cyclization of geranylgeranyl diphosphate		
CC	to casbene, a diterpene phytoalexin with antibacterial and		
CC	antifungal activity.		
CC	-!- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = casbene +		
CC	diphosphate.		
CC	-!- SUBCELLULAR LOCATION: Chloroplast.		
CC	-!- INDUCTION: By oligogalacturonide fragments released by fungal		
CC	infection. Detected after 5 h of incubation with the pectic		
CC	fragments and reaches a maximum after 10-12 h.		
CC	-!- MISCELLANEOUS: The Km of this enzyme is 1.9 micromol.		
CC	-!- SIMILARITY: Belongs to the terpene synthase family.		
CC	-!- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.		
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entities requires a license agreement (See http://www.isb-sib.ch/announce/			
or send an email to license@isb-sib.ch).			
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CC	EMBL; L32134; -; NOT ANNOTATED CDS.		
DR	InterPro; IPR008930; Terp_cyc_toroid.		
DR	InterPro; IPR001906; Terp_synth-like.		
DR	InterPro; IPR005630; Terpene_synth_C.		
DR	InterPro; IPR008949; Terpenoid_synth.		
DR	Pfam; PF01397; Terpene_synth; 1.		
DR	Pfam; PF03936; Terpene_synth; 1.		
KW	Plant defense; Lyase; Chloroplast; Transit peptide.		
FT	TRANSIT 1 56 CHLOROPLAST (POTENTIAL).		
FT	CHAIN 57 601 CASBENE SYNTHASE.		
FT	ACT_SITE 500 500 BY SIMILARITY.		
FT	ACT_SITE 575 575 BY SIMILARITY.		
FT	ACT_SITE 579 579 BY SIMILARITY.		
SQ	SEQUENCE 601 AA; 68965 MW; F7B362D286747957 CRC64;		
Query Match 20.5%; Score 667; DB 1; Length 601;			
Best Local Similarity 29.8%; Pred. No. 1.3e-37;			
Matches 174; Conservative 132; Mismatches 230; Indels 48; Gaps 19;			
QY	47	CLTSVASTDSVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMENFK	106
Db	54	CLSS--TTHQEVRLAYFPPTVWGNRF-ASLTFNPFSEFESYDERVIVLKKVKDILISST	110
QY	107	SLEDGGNDLLQRLLLVDDVERLGIDRHFKEIKTALDYV-NS---YNWEKGIGCGRESVV	162
Db	111	S-----DSVETVILIDLLCRLGVSYHFENDIEELLSKIFNSQPDLVDEK-----E	155
QY	163	TDLNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSTANIQIEGEIRGVNLFRASLVA	222
Db	156	CDLYTAAIVFRVFRQHGFKMSSDVFSKFKDSGKFES----LRGDAKGMLSLEFEASHLS	211
QY	223	FPGEKVMDEAETFSTKYLR-EALQKIPASSILSLEIRDVLEYGWHTNLPRLRARNYMDVF	281
Db	212	VHGEDILEEAFATKDYQLQSSAVELFPN---LKRHITNALAQPFHSGVPRLEARKFIDLY	268
QY	282	GQHTKNKNAAEKLELAKLEFNIFHSLQERELKHVSRWVKDSG-SPEMTFCRHRHVEYYA	340
Db	269	EADIECRN--ETLLEFAKLDYNRVQLLHQQLCQFSKWKDLNLASDIPYARDRMAEIFF	326
QY	341	LASCIAFEPQHSGRFLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSSAMECLP	400
Db	327	WAVAMYFEPDYAHTRMIIAKVLLISLIDDTIDAYATMEETHILAEAVARWDMSCLEKLP	386
QY	401	EYMKGVYMMVYHTVNEMARVAEKAQGRD-TLNYARQAWAEACFDSYMQAEAKWIATGYLPTF	459
Db	387	DYMKVIYKLLNLTTFSEFEKEL-TAEGKSYSVKYGREAFQELVRGYYLEAVWRDEGKIPSF	445
QY	460	EEYLENGKVSSAHRPCALQPILTLDIPFPDHI--LKE---VDFPSKLNLDLICIILRLRGD	514
Db	446	DDYLYNGSMTT-----GLPLVSTASFMGVQEIITGLNEFQWLETNPKLSYASGAFIRLVND	500
QY	515	TRCYKADRRAGEEASSISCYMKDNPGLTEEDALNHINFIMIRDAIRELNWELLKPDNSVPI	574
Db	501	LTSHVTEQQRGHVASCIDCYMNQH-GVSKDEAVKILQKMATDCKWKEINEECMR-QSQVSV	558
QY	575	TSKKHAFDISRVWHHGYRYRDGYSFANVETKSLVMRTVIEPVPL	618
Db	559	GHLMRIVNLARLTDVSYKYGDGYTDSQ-QLKQFVKGLFVDPI SI	601
RESULT 13			
SEAS_TOBAC			
ID	SEAS_TOBAC	STANDARD;	PRT; 548 AA.
AC	Q40577;		
DT	15-JUL-1998	(Rel. 36, Created)	









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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:39:32 ; Search time 45 Seconds  
(without alignments)  
4333.117 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRSLSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL 25:\*
- 1: sp\_archea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archheap:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3251	100.0	618	10 Q948Z0	Q948z0 abies grand
2	2416	74.3	623	10 Q94FW0	Q94fw0 abies grand
3	2328.5	71.6	629	10 Q84KL6	Q84kl6 pinus taeda
4	2266.5	69.7	627	10 Q84KL4	Q84kl4 pinus taeda
5	2264	69.6	630	10 Q9M7D1	Q9m7d1 abies grand
6	2237	68.8	634	10 Q94KA5	Q94ka5 picea abies
7	2205.5	67.8	633	10 Q94KA4	Q94ka4 picea abies
8	2163.5	66.5	627	10 Q84SM8	Q84sm8 picea abies
9	2151	66.2	628	10 Q84KL3	Q84kl3 pinus taeda
10	2137	65.7	630	10 Q9M7D0	Q9m7d0 abies grand
11	2084.5	64.1	637	10 Q9M7C9	Q9m7c9 abies grand
12	2041.5	62.8	637	10 Q94FV9	Q94fv9 abies grand
13	1985.5	61.1	615	10 Q84KL2	Q84kl2 pinus taeda
14	1909	58.7	574	10 Q84KL5	Q84kl5 pinus taeda
15	1295.5	39.8	581	10 O64404	O64404 abies grand
16	1242.5	38.2	579	10 Q94FW3	Q94fw3 abies grand

17	1240	38.1	577	10 Q94KA3	Q94ka3 picea abies
18	1231	37.9	593	10 O64405	O64405 abies grand
19	1187	36.5	782	10 Q9SAU6	Q9sau6 abies grand
20	1187	36.5	817	10 O81086	O81086 abies grand
21	1178.5	36.3	816	10 Q94FW2	Q94fw2 abies grand
22	1131	34.8	873	10 Q947C4	Q947c4 ginkgo bilo
23	1055.5	32.5	853	10 Q94FW1	Q94fw1 abies grand
24	1052.5	32.4	868	10 Q38710	Q38710 abies grand
25	836	25.7	603	10 Q8GUE4	Q8gue4 cinnamomum
26	824	25.3	606	10 O8L5K3	O8l5k3 citrus limo
27	821	25.3	606	10 O8L5K1	O8l5k1 citrus limo
28	812	25.0	597	10 Q93X23	Q93x23 quercus ile
29	796.5	24.5	595	10 Q9AR86	Q9ar86 populus x c
30	794.5	24.4	595	10 Q7XAS7	Q7xas7 populus tre
31	765.5	23.5	606	10 Q8H2B4	Q8h2b4 mentha aqua
32	757	23.3	576	10 Q84LB2	Q84lb2 malus domes
33	749.5	23.1	582	10 Q94G53	Q94g53 artemisia a
34	747.5	23.0	607	10 Q8W1J9	Q8wlj9 perilla fru
35	744	22.9	613	10 Q940E7	Q940e7 agastache r
36	742	22.8	583	10 Q7Y1V1	Q7y1v1 melaleuca a
37	736.5	22.7	598	10 O81192	O81192 salvia offi
38	732	22.5	583	10 Q9SPN1	Q9spn1 artemisia a
39	728.5	22.4	567	10 Q9SPN0	Q9spn0 artemisia a
40	727	22.4	620	10 Q9FUW5	Q9fuw5 schizonepet
41	724.5	22.3	599	10 Q40322	Q40322 mentha spic
42	721	22.2	597	10 O8L5J7	O8l5j7 salvia sten
43	717.5	22.1	599	10 Q9SW76	Q9sw76 mentha long
44	710.5	21.9	551	10 Q9LKN1	Q9lkn1 gossypium h
45	710.5	21.9	603	10 O04806	O04806 perilla fru

ALIGNMENTS

RESULT 1

- Q948Z0
- ID Q948Z0 PRELIMINARY; PRT; 618 AA.
- AC Q948Z0;
- DT 01-DEC-2001 (TrEMBLrel. 19, Created)
- DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
- DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
- DE (-)-camphene synthase.
- GN AG6.5.
- OS Abies grandis (Grand fir).
- OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
- OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
- OX NCBI\_TaxID=46611;
- RN [1]
- RP SEQUENCE FROM N.A.
- RX MEDLINE=97413772; PubMed=9268308;
- RA Bohlmann J., Steele C.L., Croteau R.;
- RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
- RL J. Biol. Chem. 272:21784-21792(1997).
- RN [2]
- RP SEQUENCE FROM N.A.
- RX MEDLINE=99373092; PubMed=10441373;
- RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;
- RT "cDNA cloning, characterization, and functional expression of four new monoterpene synthase members of the Tpsd gene family from grand fir (Abies grandis).";
- RL Arch. Biochem. Biophys. 368:232-243(1999).
- DR EMBL; U87910; AAB70707.1; -;
- DR GO; GO:0016829; F:lyase activity; IEA.
- DR GO; GO:0008152; P:metabolism; IEA.
- DR InterPro; IPR005630; Terpene\_synth\_C.
- DR InterPro; IPR008949; Terpenoid\_synth.
- DR InterPro; IPR008930; Terp\_cyc\_toroid.
- DR InterPro; IPR001906; Terp\_synth-like.
- DR Pfam; PF01397; Terpene\_synth; 1.
- DR Pfam; PF03936; Terpene\_synth\_C; 1.
- SQ SEQUENCE 618 AA; 70749 MW; B07B5185CE5C4CE1 CRC64;

Query Match 100.0%; Score 3251; DB 10; Length 618;  
Best Local Similarity 100.0%; Pred. No. 9e-232;  
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLSITPLVSRSCSSSHEIKALRRRTIPTLIGICRPGKSVASHSINMCLTSVASTDSVQRR 60  
DB 1 MALLSITPLVSRSCSSSHEIKALRRRTIPTLIGICRPGKSVASHSINMCLTSVASTDSVQRR 60

QY 61 VGNYSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGGNDLLQRL 120  
DB 61 VGNYSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGGNDLLQRL 120

QY 121 LVDDVERLGDIDRHFKKEIKTALDYVNSYWNKGGIGCGRESVVTDLNSTALGLRTLRLHG 180  
DB 121 LVDDVERLGDIDRHFKKEIKTALDYVNSYWNKGGIGCGRESVVTDLNSTALGLRTLRLHG 180

QY 181 TVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGKVMDEAETFTSKYL 240  
DB 181 TVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGKVMDEAETFTSKYL 240

QY 241 REALQKIPASSILSLEIRDVLEYGWHTNLPRLARNYMDVFGQHTKNKNAEKLLELAKL 300  
DB 241 REALQKIPASSILSLEIRDVLEYGWHTNLPRLARNYMDVFGQHTKNKNAEKLLELAKL 300

QY 301 EFNIFHSLQERELKHVSRRWKDGSPEMTFCRHRHVEYYALASCIAPFQHSGLGFTK 360  
DB 301 EFNIFHSLQERELKHVSRRWKDGSPEMTFCRHRHVEYYALASCIAPFQHSGLGFTK 360

QY 361 MSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVMMVYHTVNEARV 420  
DB 361 MSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVMMVYHTVNEARV 420

QY 421 AEKAQGRDTLNYARQAEACFDSYMQEAKWIATGYLPTFEEYLENGKVSSAHRPCALQPI 480  
DB 421 AEKAQGRDTLNYARQAEACFDSYMQEAKWIATGYLPTFEEYLENGKVSSAHRPCALQPI 480

QY 481 LTLDIPFPDHILKEVDFFPSKNDLICIILRLRGDTRCYKADRARGEAEASSISCYMKDNP 540  
DB 481 LTLDIPFPDHILKEVDFFPSKNDLICIILRLRGDTRCYKADRARGEAEASSISCYMKDNP 540

QY 541 LTEDALNHINFMRDAIRELNWELLKPDNSVPITSKKHAFDISRVVHHGYRVDGYSEA 600  
DB 541 LTEDALNHINFMRDAIRELNWELLKPDNSVPITSKKHAFDISRVVHHGYRVDGYSEA 600

QY 601 NVETKSLVMRTVIEPVPL 618  
DB 601 NVETKSLVMRTVIEPVPL 618

RESULT 2  
Q94FW0  
ID Q94FW0 PRELIMINARY; PRT; 623 AA.  
AC Q94FW0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Pinene synthase (Fragment).  
OS Abies grandis (Grand fir).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferales; Pinaceae; Abies.  
OX NCBI\_TaxID=46611;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21297238; PubMed=11404343;  
RA Trapp S.C., Croteau R.B.;  
RT "Genomic organization of plant terpene synthases and molecular  
evolutionary implications."  
RL Genetics 158:811-832(2001).  
DR EMBL; AF326517; AAK83564.1; --  
DR GO; GO:0016829; F-lyase activity; IEA.  
DR GO; GO:0008152; P-metabolism; IEA.  
DR InterPro; IPR005630; Terpene\_synth\_C.

DR InterPro; IPR008949; Terpenoid\_synth.  
DR InterPro; IPR008930; Terp\_cyc\_toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR Pfam; PF01397; Terpene\_synth; 1.  
DR Pfam; PF03936; Terpene\_synth\_C; 1.  
FT NON TER 1  
SQ SEQUENCE 623 AA; 70948 MW; 823B82B38113467B CRC64;

Query Match 74.3%; Score 2416; DB 10; Length 623;  
Best Local Similarity 74.8%; Pred. No. 5.2e-170;  
Matches 467; Conservative 59; Mismatches 82; Indels 16; Gaps 6;

QY 8 PLVSRCL-----SSSHEIKALRRRTIPTLIGICRPGKSVASHSINMCLTSVASTDSVQRRVG 62  
DB 3 PLAKSCLHKSLISSSTHELKALSRTPALGMSRRGKSITPSISMSSTVVTDDGVRRRMG 62

QY 63 NYHSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGG-----NDLLQ 117  
DB 63 DFHSNLWDDDFIQSL-PTAYEEKSYLERAEKLI GEVEN-MENMSLEDGELMSPLNDLIQ 120

QY 118 RLLLVDDVERLGDIDRHFKKEIKTALDYVNSYWNKGGIGCGRESVVTDLNSTALGLRTLRL 177  
DB 121 RLWIVDSLGRGLIHRHFKDEIKSALDYVSYWGENGIGCGRESAVTDLNSTALGFRTLRL 180

QY 178 HGTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGKVMDEAETFTST 237  
DB 181 HGVPSDDVFKAFKQNGQFSCSENIQTDEEIRGVNLFRASLIAPFGEKIMDEAEIFST 240

QY 238 KYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLARNYMDVFGQHTKNKNA---AEKL 294  
DB 241 KYLKEALQKIPVSS-LSREIGDVLGYGHTYLPRLARNYIHVFGQDTENTKSYVKS KL 299

QY 295 LELAKLEFNIFHSLQERELKHVSRRWKDGSPEMTFCRHRHVEYYALASCIAPFQHSGLG 354  
DB 300 LELAKLEFNIFQSLQKRELSVRWWKESGFPEMTFCRHRHVEYYTLASCIAPFQHSGLG 359

QY 355 RLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVMMVYHTV 414  
DB 360 RLGFAKTCHLITVLDMDYDVGTVDELELFTATIKRWDPSIDCLPEYMKGVYIAVDTV 419

QY 415 NEMARVAEKAQGRDTLNYARQAEACFDSYMQEAKWIATGYLPTFEEYLENGKVSSAHRP 474  
DB 420 NEMAREAEAAQGRDTLYAREAEAYIDSYMQEAKWIATGYLPSDFEYENGKVCGRHRI 479

QY 475 CALQPILTLDIPFPDHILKEVDFFPSKNDLICIILRLRGDTRCYKADRARGEAEASSISCY 534  
DB 480 SALQPILTMDIPFPDHILKEVDFFPSKNDLACAILRLRGDTRCYKADRARGEAEASSISCY 539

QY 535 MKDNPGLTEEDALNHINFMRDAIRELNWELLKPDNSVPITSKKHAFDISRVVHHGYR 594  
DB 540 MKDNPGVSEEDALDHINAMISDVIGLWELLKPDINVPISAKKHAFDIARAFHYGYK 599

QY 595 DGYSEANVETKSLVMRTVIEPVPL 618  
DB 600 DGYSEANVETKSLVTRTLLESVPL 623

RESULT 3  
Q84KL6  
ID Q84KL6 PRELIMINARY; PRT; 629 AA.  
AC Q84KL6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE (-)-alpha-pinene synthase.  
OS Pinus taeda (Loblolly pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=3352;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22510022; PubMed=12623076;  
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;



ID Q9M7D1 PRELIMINARY; PRT; 630 AA.  
AC Q9M7D1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Beta-phellandrene synthase.  
GN AGC8.  
OS Abies grandis (Grand fir).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.  
OX NCBI\_TaxID=46611;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Stem;  
RX MEDLINE=99373092; PubMed=10441373;  
RA Bohlmann J., Phillips M., Ramachandiran V., Katch S., Croteau R.;  
RT "cDNA cloning, characterization, and functional expression of four new  
RT monoterpene synthase members of the Tpsd gene family from grand fir  
RT (Abies grandis).";  
RL Arch. Biochem. Biophys. 368:232-243 (1999).  
DR EMBL; AF139205; AAF61453.1; -.  
DR HSSP; Q40577; 5EAU.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR005630; Terpene synth C.  
DR InterPro; IPR008949; Terpenoid synth.  
DR InterPro; IPR008930; Terp\_cyc toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR Pfam; PF01397; Terpene synth; 1.  
DR Pfam; PF03936; Terpene synth C; 1.  
SQ SEQUENCE 630 AA; 72784 MW; B8E4374B262FF2D1 CRC64;  
  
Query Match 69.6%; Score 2264; DB 10; Length 630;  
Best Local Similarity 68.3%; Pred. No. 9.2e-159;  
Matches 435; Conservative 78; Mismatches 98; Indels 26; Gaps 9;  
  
QY 1 MALLSITPLVSRSL-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVAST 54  
Db 1 MALVSSAP---KSLCHKSLIRSTHHELKPLRRTIPTLGMCRRGKSFTPSVMSLTTAVSD 57  
  
QY 55 DSVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGG-- 112  
Db 58 DGLQRRIGDYHNSLWDDDFIQSL-STPYGEPYSYRERAEKLI GEVKE-MFNMSPSDGE SM 115  
  
QY 113 ---NDLLQRLLLVDVVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTA 169  
Db 116 SPLNDLIERLWMVDSVERLIGIDRHFKKEIKSALDYVSYWNKEGIGCGRDSVFDPVNSTA 175  
  
QY 170 LGLRTLRLHGYTVSSDVNLNVFKDKNGQFSSTANIQTIEGEIRGVNLFRASLVAFPGKVM 229  
Db 176 SGFRTLRLHGYSVSSEVLKVFDQNGQFAFSPSTK-ERDRTVNLNLYRASFIAPFGKVM 234  
  
QY 230 DEAEFTSTKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLRNMYMDVFGQHT---- 285  
Db 235 EEAEIFSSRYLKEAVQKIPVSS-LSQEI DYTLEYGWHNTMPRLNLYLDVFGHPTSPWL 293  
  
QY 286 KNKNA----AEKLLLELAKLEFNIFHSLQERELKHVSRWWKDSGSPMTFCRHRHVEYYAL 341  
Db 294 KKKRTQYLDSEKLLLELAKLEFNIFHSLQKELQVLSRWIHSGLPELTFGRHHRHVEYYTL 353  
  
QY 342 ASCIAFEPQHSGERLGTQKMSHLITVLDMDYVFGTVDELELFTATIKRWDP SAMECLPE 401  
Db 354 SSCIA TEPKHSAFRLGPAKTCHLITVLD DDIYDTFGTMDEIELFN EAVRRWNPSEKERLPE 413  
  
QY 402 YMKGVYMMVYHTVNMARVAEKAQGRD TLNLYARQAEACFDSYMQEAKWIATG YLPTFEE 461  
Db 414 YMKEIYMALYEALTMAREAEK TQGRD TLNLYARKAWEVYLD SYTQEA KWIASGYLPTFEE 473  
  
QY 462 YLENGKVSSAHRPCALQPLITLDIPFPD HILKEVDFPSKNDLICIILRLRGDTRCYKAD 521  
Db 474 YLENAKVSSGHRAAALTPLLTLDPVPLPDDVLKGIDFPSPSRFNDLASSFLRLRGDTRCYKAD 533  
  
QY 522 RARGEAEASSISCYMKDNPGLTEEDALNHINFMRDAIR ELNWLKPDNSVPI TSKKHAF 581

Db 534 RDRGEEASSISCYMKDNPGLTEEDALNHINAMINDI IKELNWE L LKPD SNIPMTARKHAY 593  
  
QY 582 DISRVVHHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618  
Db 594 EITRAFHLQLYKYRDGFSVATQETKSLVRRTVLEPVPL 630  
  
RESULT 6  
Q94KA5  
ID Q94KA5 PRELIMINARY; PRT; 634 AA.  
AC Q94KA5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Beta-phellandrene synthase-like protein.  
OS Picea abies (Norway spruce) (Picea excelsa).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
OX NCBI\_TaxID=3329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Morency M.J., Nicole M.C., Seguin A.;  
RT "Terpene synthase from Norway spruce, cDNA isolation and  
RT characterization of beta-phellandrene synthase-like gene.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF369918; AAK39127.2; -.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR005630; Terpene synth C.  
DR InterPro; IPR008949; Terpenoid synth.  
DR InterPro; IPR008930; Terp\_cyc toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR Pfam; PF01397; Terpene synth; 1.  
DR Pfam; PF03936; Terpene synth C; 1.  
SQ SEQUENCE 634 AA; 72768 MW; EE140A49C46B4404 CRC64;  
  
Query Match 68.8%; Score 2237; DB 10; Length 634;  
Best Local Similarity 68.0%; Pred. No. 9.2e-157;  
Matches 434; Conservative 75; Mismatches 105; Indels 24; Gaps 10;  
  
QY 1 MALLSITPLVSRSL-----SSSHEIKALRRTIPTLGICRPGKSV A-HSINMCLT-SVAS 53  
Db 1 MSPVSVIPLAYKLC LPRSLMSSSREV KPLHITIPNLGMCRRGKSMAPASTSMILTA AVSD 60  
  
QY 54 TDSVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGG- 112  
Db 61 DDRVQRRRGVHNSLWDDDFIQSL-STPYGEPYSYRERAE TLKGEIKK-MFRSISKDDGEL 118  
  
QY 113 ---NDLLQRLLLVDVVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNST 168  
Db 119 ITPNLNDLIQRLWMVDSVERLIGIDRHFKKEIKSALDYVSYWNKEGIGCGRDSVVADLNST 178  
  
QY 169 ALGLRTLRLHGYTVSSDVNLNVFKDKNGQFSSTANIQTIEGEIRGVNLFRASLVAFPGK V 228  
Db 179 ALGFRTLRLHGYTVSSEVLKVFDQNGQFACSPS-KTEGEIR S ALNLYRASLIAPFGK V 237  
  
QY 229 MDEAETFTKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLRNMYMDVFGQHT--- 285  
Db 238 MDDAEIFSSRYLKEAVQKIPDCS-LSQEIAYALEY GWHNTMPRLRNMYMDVFGHPSSPW 296  
  
QY 286 --KNKNA---AEKLLLELAKLEFNIFHSLQERELKHVSRWWKDSGSPMTFCRHRHVEYYA 340  
Db 297 LKKNKTYMDGKELLELAKLEFNIFHSLQEEELQYISRWWKDSGLPKLAFSRHRHVEYYT 356  
  
QY 341 LASCIAFEPQHSGERLGTQKMSHLITVLDMDYVFGTVDELELFTATIKRWDP SAMECLP 400  
Db 357 LGSCIATDPKHRAFRLGFVKTCHLNTVLDDIYDTFGTMDEIELFTEAVRRWDPSETESLP 416  
  
QY 401 EYMKGVYMMVYHTVNMARVAEKAQGRD TLNLYARQAEACFDSYMQEAKWIATG YLPTFE 460  
Db 417 DYMKGVYMYVLYEALTEMAQEAKTQGRD TLNLYARKAWEIYLD SYIQEAKWIATGYLPTFQ 476





Db 238 EAEIFSATYLKEALQTIPIVSS-LSQEIQYVLQYRWHSNLPRLREARTYIDILQENTKNQML 296  
QY 291 ---AEKLELAKLEFNIFHSLQERELKHVSRWKDSGSPEMTFCRHRHVEYYALASCI AF 347  
Db 297 DVNTKKVLELAKLEFNIFHSLQNELKSVSRWWKESGFPDLNFIRHRHVEFYTLVSGIDM 356  
QY 348 EPQHSGRFGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSPAMECLPEYMKGVY 407  
Db 357 EPKHCTFRLSFVKMCHLITVLDDMYDTFGTIDELRLFTA AVKRWDPSTTECLPEYMKGVY 416  
QY 408 MMVYHTVNMARVAEKAQGRDITLNYARQAEACFDSYMQEAKWIA TGILPTFEEYLENGK 467  
Db 417 TVLYETVNEMAEQAQKSQGRDITLSYVRQALEAYIGAYHKEAEWISSGYLPTFDEYFENGK 476  
QY 468 VSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNLDLICIILRLRGDTRCYKADRAGEE 527  
Db 477 VSSGHRIATLQPTFMLDIPFPHHVLQEI DFPSKFNDFA CSILRLRGDTRCYQADRAGEE 536  
QY 528 ASSISCYMKDNPGLTTEEDALNHINFMRDAIRELNWELLKPDNSVPITSKKHAFDISRVW 587  
Db 537 ASCISCYMKDNPGSTQEDALNHINNMIETIKKLNWELLKPDNNVPISSKKHAFDINRGL 596  
QY 588 HHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618  
Db 597 HHFYNYRDGYTVASNETKNLVIKTVLEPVPM 627

RESULT 9

Q84KL3 ID Q84KL3 PRELIMINARY; PRT; 628 AA.  
AC Q84KL3;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE (+)-alpha-pinene synthase.  
OS Pinus taeda (loblolly pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=3352;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22510022; PubMed=12623076;  
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;  
RT "CDNA isolation, functional expression, and characterization of (+)-  
RT alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine  
RT (Pinus taeda): Stereococontrol in pinene biosynthesis.";  
RL Arch. Biochem. Biophys. 411:267-276(2003).  
DR EMBL; AF543530; AA061228.1; -.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR005630; Terpene synth C.  
DR InterPro; IPR008949; Terpenoid synth.  
DR InterPro; IPR008930; Terp\_cyc\_toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR Pfam; PF01397; Terpene\_synth; 1.  
DR Pfam; PF03936; Terpene synth C; 1.  
SQ SEQUENCE 628 AA; 71495 MW; 4208222612256837 CRC64;

Query Match 66.2%; Score 2151; DB 10; Length 628;  
Best Local Similarity 65.8%; Pred. No. 2.1e-150;  
Matches 416; Conservative 92; Mismatches 106; Indels 18; Gaps 8;

QY 1 MALLSITPLVSRSL-----SSSHEIKALRRPTLTGICRPGKSVAH SINM-CLTSVAST 54  
Db 1 MALVSAVPLNSKLCURRTLFGFSHELKAIHSTVPLNLCMCRGGKSIAPSMSTTSVSNE 60  
QY 55 DSVQRRVGNVYHNSLWDDDFIQSLISTPYGADPYRERADRLIGEVDIMFNFKSLEDGG-- 112  
Db 61 DGVPRRIAGHHSNLWDDDSIASL-STSYEAPSYRKRADKLIGEVKNI-FDLMSVEDGVFT 118  
QY 113 ---NDLLQRLLLVDDVERLIGIDRHFHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTA 169  
Db 119 SPLSDLHRLMWVDSVERLIGIDRHFHFKDEINSALDHVYSYWTEKGIGRGESGVTDLNSTA 178

QY 170 LGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLNFRASLVAFPGEKVM 229  
Db 179 LGLRTLRLHGYTVSSHVLDFHFKNEKGQFTCSA-IQTEGEIRDVLNFRASLIAFPGEKIM 237  
QY 230 DEAEFTSTKYLRBALQKIPASSILSLEIRDVLBYGWHNTNLPRLREARNYMDVFGQHTKNKN 289  
Db 238 EAAEIFSTMVYLKDALKQIPPSG-LSQEIEYLLEFGWHNTNLPRLMETRMVYIDVFGEDTTFET 296  
QY 290 ---AAEKLELAKLEFNIFHSLQERELKHVSRWKDSGSPEMTFCRHRHVEYYALASCI A 346  
Db 297 PYLIREKLELAKLEFNIFHSLVKRELQSLRSRWKDYGFPEITFSRHRHVEYYTLAACIA 356  
QY 347 FEQHSGRFGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSPAMECLPEYMKGV 406  
Db 357 NDPKHSAFRLGFGKISHMITILDDIYDTFGTMEELKLLTA AFKRWDPSSIECLPDYMKGV 416  
QY 407 YMMVYHTVNEMARVAEKAQGRDITLNYARQAEACFDSYMQEAKWIA TGILPTFEEYLENG 466  
Db 417 YMAVYDNINEMAREAQIQGWDITVSYARKSWEAFIGAYIQEAKWISSGYLPTFDEYLENG 476  
QY 467 KVSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNLDLICIILRLRGDTRCYKADRAGE 526  
Db 477 KVSFGSRITTLPEMLTLGFPPLPRILQEI DFPSKENDLICAILRLKGTQCYKADRAGE 536  
QY 527 EASSISCYMKDNPGLTTEEDALNHINFMRDAIRELNWELLKPDNSVPITSKKHAFDISRV 586  
Db 537 EASAVSCYMKDHPGITEEDAVNQVNAMVDNLTKELNWELLRPDSGVPISYKKVAFDICRV 596  
QY 587 WHHGYYRYRDGYSFANVETKSLVMRTVIEPVPL 618  
Db 597 FHYGYKYRDGFSVASIEIKNLVTRTVVETVPL 628

RESULT 10

Q9M7D0 ID Q9M7D0 PRELIMINARY; PRT; 630 AA.  
AC Q9M7D0;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Terpinolene synthase.  
GN AGC9.  
OS Abies grandis (Grand fir).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.  
OX NCBI\_TaxID=46611;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Stem;  
RX MEDLINE=99373092; PubMed=10441373;  
RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;  
RT "CDNA cloning, characterization, and functional expression of four new  
RT monoterpane synthase members of the Tpsd gene family from grand fir  
RT (Abies grandis).";  
RL Arch. Biochem. Biophys. 368:232-243(1999).  
DR EMBL; AF139206; AAF61454.1; -.  
DR HSSP; Q40577; SEAU.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR005630; Terpene synth C.  
DR InterPro; IPR008949; Terpenoid synth.  
DR InterPro; IPR008930; Terp\_cyc\_toroid.  
DR InterPro; IPR001906; Terp\_synth-like.  
DR Pfam; PF01397; Terpene synth; 1.  
DR Pfam; PF03936; Terpene synth C; 1.  
SQ SEQUENCE 630 AA; 72508 MW; 452437B87F203D8A CRC64;

Query Match 65.7%; Score 2137; DB 10; Length 630;  
Best Local Similarity 67.4%; Pred. No. 2.3e-149;  
Matches 427; Conservative 73; Mismatches 114; Indels 20; Gaps 9;

QY 1 MALLSITPLVSRSLS----SSSHEIKALRRPTLTGICRPGKSVAH SINMCLTSVASTD 55

Db 1 MALVSILPLSSKSVLHKSWIVSTYEHKAISRTIPNLGLRGRKSVTHSRMSLSTAVSDD 60

QY 56 -SVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNKSLSDGG-- 112

Db 61 HGVQRRIVEFHSNLWDDDFIQSL-STPYGAPSYRERADRLIVEVKGI-FTSISAEDGELI 118

QY 113 ---NDLLQRLLLVDDVERLIGIDRHFKEIKTALDYVNSYWNKGGIGCGRESVVTDLNSTA 169

Db 119 TPLNDLIQRLLMVDNVERLIGIDRHFKEIKAAALDYVSYWNKGGIGCGSDSGVADLNSTA 178

QY 170 LGLRTLRLHGYTVSSDVLNVFKD--KNGQFSSTANIQIEGEIRGVNLFRASLVAFPGEK 227

Db 179 LGRILRLHGYSVSSDVLNHFKEEKEKGQFVCSA-IQTEEEIKSVNLFRASLIAFPGEK 237

QY 228 VMDEAETFTSKYLREALQKIPASSILSLEIRDVLEYGWHNTLPRLEARNYMDVFGQHTKN 287

Db 238 VMEEAEIFSKIYLKEALQNIAVSS-LSREIEYVLEDGWQTNMPRLTRNYIDVLGENDRD 296

QY 288 KNA---AEKLLLELAKLEFNIHLSQERELKHVSRWWKDSGSPMTFCRRHVEYYALASC 344

Db 297 ETLYMNMEKLLLEIAKLEFNIHLSQERELKDLRWWKDSGFSHLTFSRHRHVEFYALASC 356

QY 345 IAFEPQHSGFRLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPNAMECLPEYMK 404

Db 357 IETDRKHSGRFLGPAKWMCHLITVLDDIYDTFCITMEELELFTAFAKRWDPESATDLLPEYMK 416

QY 405 GVYMMVYHTVNEMARVAEKAQGRDRTLNYARQAWAEACFDSYMQEAKWIATGYLPTFEEYLE 464

Db 417 GLYMMVYETVNEIAREADKSKQRETLDNDRARAWAYLDSYMKAEAWISSGYLPTFEEYME 476

QY 465 NGKVSSAHRPCALQPILTLDIPFPDHILKEVDFPPSKLNDLICIILRLGDRTRCYKADRAR 524

Db 477 TSKVSFGYRIFALQPILTMDVPLTHHILQEIQDFPLRFNDLICSILRLKNDTRCYKADRAR 536

QY 525 GEEASSISCYMKNDPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDIS 584

Db 537 GEEASCISCYMKENPGSTEEDAINHINAMVNLIKEVNWELLRQDGTAKHAFDIL 596

QY 585 RVWHHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618

Db 597 KGS LHGYKYRDGYSFANVETKSNVVRTVLESVPL 630

RESULT 11

Q9M7C9 ID Q9M7C9 PRELIMINARY; PRT; 637 AA.

AC Q9M7C9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE (-)-limonene/(-)-alpha-pinene synthase.

GN AGC11.

OS Abies grandis (Grand fir).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.

OX NCBI\_TaxID=46611;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=stem;

RX MEDLINE=99373092; PubMed=10441373;

RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;

RT "cDNA cloning, characterization, and functional expression of four new

RT monoterpene synthase members of the Tpsd gene family from grand fir

RT (Abies grandis).";

RL Arch. Biochem. Biophys. 368:232-243 (1999).

DR EMBL; AF139207; AAF61455.1; -.

DR HSSP; Q40577; SEAS.

DR GO; GO:0016829; F:lyase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR005630; Terpene synth C.

DR InterPro; IPR008949; Terpenoid synth.

DR InterPro; IPR008930; Terp\_cyc\_toroid.

DR InterPro; IPR001906; Terp synth-like.

DR Pfam; PF01397; Terpene synth; 1.

DR Pfam; PF03936; Terpene synth C; 1.

SQ SEQUENCE 637 AA; 73273 MW; B3574986FEC96CFB CRC64;

Query Match 64.1%; Score 2084.5; DB 10; Length 637;

Best Local Similarity 64.9%; Pred. No. 1.8e-145;

Matches 417; Conservative 80; Mismatches 115; Indels 31; Gaps 13;

QY 1 MALLSITPL-VSRSC----LSSSHEIKAL--RRTIPTLGICRPGKSVAHNSINMCLTSTA 52

Db 1 MALLSIVSLQVPKSCGLKSLISSNVQKALCISTAVPTLRMRRRQKALV--INMKLTTS 58

QY 53 STDS-----VQRRVGNVHNSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNF-- 105

Db 59 HRDDNGGGVQLORRIADHHPNLWEDDFIQSL-SSPYGSSYSERAVTVVEEVKE-MFNSIP 116

QY 106 --KSLEDGGNDLLQRLLLVDDVERLIGIDRHFKEIKTALDYVNSYWNK-GIGCGRESV 162

Db 117 NNRELFQSQNDLLTRLMMVDSIERLIGIDRHFQNEIRVALDYVSYWKEKEGIGCGRDS 176

QY 163 TDLNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEI-RGVNLFRASLV 221

Db 177 PDLNSTALALETLRLHGYNVSSDVLVEYFKDKQGHFACPA-ILTEGQITRSVNLRYASLV 235

QY 222 AFPGEKVMDEAETFTSKYLREALQKIPASSILSLEIRDVLEYGWHNTLPRLEARNYMDVF 281

Db 236 AFPGEKVMEEAIFASLYLKEVLQKIPVSS-FSREIEYVLEYGWHNTLPRLEARNYIDVY 294

QY 282 QGHTKNKN-----AAEKLLELAKLEFNIHLSQERELKHVSRWWKDSGSPMTFCRRH 335

Db 295 GDYSYESSNEMPVNTQKLLKLEFNIHLSQKELQYISRWKDKSCSSHLTFTTRHRH 354

QY 336 VEYALASCTAFEPQHSGFRLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDP 395

Db 355 VEYITWASCISMPEPKHSAFRLGFTKCHLLTVLDDMYDTFGTLDLQLETTAFKRWDLSE 414

QY 396 MECLPEYMKGYMMVYHTVNEMARVAEKAQGRDRTLNYARQAWAEACFDSYMQEAKWIATGY 455

Db 415 TKCLPEYMKAVYMDLYQCLNELAQEAETQGRDRTLNYIRNAYESHFDSFMHEAKWISSGY 474

QY 456 LPTFEEYLENGKVSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNLDLICIILRLGDT 515

Db 475 LPTFEEYLNKGVSSGSRATATLQPILTLDVPLPNYILQEIIDYPSRFNDLASSLLRLGDT 534

QY 516 RCYKADRARGEAEASSISCYMKNDPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPIT 575

Db 535 RCYKADRARGEAEASAIACYMKDHPGSTEEDALNHINVMISDAIRELNWELLRPDSKSPIS 594

QY 576 SKKHAFDISRVWHHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618

Db 595 SKKHAFDITRAFPHLYKYRDGYTVASSETKNLVMKTVLEPVAL 637

RESULT 12

Q94FV9 ID Q94FV9 PRELIMINARY; PRT; 637 AA.

AC Q94FV9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE (-)-4S-limonene synthase.

OS Abies grandis (Grand fir).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.

OX NCBI\_TaxID=46611;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21297238; PubMed=11404343;

RA Trapp S.C., Croteau R.B.;

RT "Genomic organization of plant terpene synthases and molecular

RT evolutionary implications.;"

RL Genetics 158:811-832 (2001).







DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE	Alpha-farnesene synthase.
OS	Pinus taeda (loblolly pine).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX	NCBI_TaxID=3352;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22510022; PubMed=12623076;
RA	Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT	"cdna isolation, functional expression, and characterization of (+)-
RT	alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine
RT	(Pinus taeda): Stereococontrol in pinene biosynthesis.";
RL	Arch. Biochem. Biophys. 411:267-276(2003).
DR	EMBL; AF5433528; AAC61226.1; -.
DR	GO; GO:0016829; F:lyase activity; IEA.
DR	GO; GO:0008152; P:metabolism; IEA.
DR	InterPro; IPR005630; Terpene synth C.
DR	InterPro; IPR008949; Terpenoid synth.
DR	InterPro; IPR008930; Terp_cyc toroid.
DR	InterPro; IPR001906; Terp_synth-like.
DR	Pfam; PF01397; Terpene_synth; 1.
DR	Pfam; PF03936; Terpene_synth_C; 1.
SQ	SEQUENCE 574 AA; 65941 MW; 26746BAE32ACF19A CRC64;
Query Match 58.7%; Score 1909; DB 10; Length 574;	
Best Local Similarity 63.3%; Pred. No. 1.5e-132;	
Matches 366; Conservative 88; Mismatches 110; Indels 14; Gaps 8;	
QY	50 SVASTDSVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEYKDIMFNFKSLE 109
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QY	110 DGGNDL---LQRLLLVDDVERLGIDRHFKKEIKTALDYVNS--YWNKEGIGCGRESVWTDL 165
Db	60 DGDDEICYFLQRLWMIDNVERLGISRHFENEIKAAMEDVYSRHWSDKGIACGRHSWADL 119
QY	166 NSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPG 225
Db	120 NSTALAFRTLRLHGYSCVSDVFKIFQDQGEFACSAQ-QTEGEIKGILNLLRASLIAFPG 178
QY	226 EKMDEAETFSKYLREALQKIPASSILSLERDVLEYGWHTNLPRLRNMDVDFGQH- 284
Db	179 ERILQEAEIFATYLKEALPKIQGSR-LSQETEVVLEYGWLTDLPRLTRNVIIEVLAEEI 237
QY	285 ----TKNKNAAEKLLLELAKLEFNIFHSLQERELKHVSRWWKDSGSPMTFCRRHRHVEYYA 340
Db	238 TPYFKKPCMAVEKLLKLAKIEFNLFHSLQTELKHLRWWKDSGFAQLTFRHRHVEFYT 297
QY	341 LASCIAFEPQHSGERLGTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLP 400
Db	298 LASCIAMEPKHSAFRLGFAKLCYLGIVLDDIYDTYGMKEELELFTAAIKRWDSTTECLP 357
QY	401 EYMGVYMMVYHTVNEMARVAEKAQGRDITLNYARQAWAEACFDSYMQEAKWIATGYLPTFE 460
Db	358 EYMGVYMAFYDCVNEMARQAETQGWDTLDYARKTWEALIDAFMEEAkWISSGYVPTFQ 417
QY	461 EYLENGKVSSAHRPCALQPILTDIPFPDHILKEVDFFPSKLNLDLICIILRLRGDTRCYKA 520
Db	418 KYLDNGKVSFGYRAATLQPILTDIPLPLHLIQEIDFPSSFNDLASSILRLRGDICYQA 477
QY	521 DRARGEAEASSISCYMKDNPGLTEEDALNHINFMIRDARELNWELLKPDNSVPITSKKHA 580
Db	478 ERSRGEQASSISCYMKDNPGSTEEEDALSHVNAMIGDKIPEFNWFEWFKP-SKAPISSKKYA 536
QY	581 FDISRVVWHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
Db	537 FDILRAFYHLYKYRDGFGFSIAKIETKKLVMRVTLPDVPVM 574
RESULT 15	
O64404	
ID	O64404 PRELIMINARY; PRT; 581 AA.

AC	O64404;
DT	01-AUG-1998 (TReMBLrel. 07, Created)
DT	01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE	D-selinene synthase.
OS	Abies grandis (Grand fir).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX	NCBI_TaxID=46611;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98113169; PubMed=9442047;
RA	Steele C.L., Crock J., Bohlmann J., Croteau R.;
RT	"Sesquiterpene synthases from grand fir (Abies grandis). Comparison of
RT	constitutive and wound-induced activities, and cdna isolation,
RT	characterization, and bacterial expression of delta-selinene synthase
RT	and gamma-humulene synthase.";
RL	J. Biol. Chem. 273:2078-2089(1998).
DR	EMBL; U92266; AAC05727.1; -.
DR	HSSP; Q40577; 5EAU.
DR	GO; GO:0016829; F:lyase activity; IEA.
DR	GO; GO:0008152; P:metabolism; IEA.
DR	InterPro; IPR005630; Terpene synth C.
DR	InterPro; IPR008949; Terpenoid synth.
DR	InterPro; IPR008930; Terp_cyc toroid.
DR	InterPro; IPR001906; Terp_synth-like.
DR	Pfam; PF01397; Terpene_synth; 1.
DR	Pfam; PF03936; Terpene_synth_C; 1.
SQ	SEQUENCE 581 AA; 67967 MW; 8646222AB8BCC32C8 CRC64;
Query Match 39.8%; Score 1295.5; DB 10; Length 581;	
Best Local Similarity 44.1%; Pred. No. 3.5e-87;	
Matches 255; Conservative 118; Mismatches 190; Indels 15; Gaps 8;	
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QY	113 NDLLQRLLLVDDVERLGIDRHFKKEIKT-ALDYVNSYWNKEGIGCG-RESVVTDLNSTAL 170
Db	64 HDLIKRLQIVDTLECLGIDRHFEHEIQTAALDYVYRWNNKEGIGESRDSFSKDLNATAL 123
QY	171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEG----EIRGVNLFRASLVAFPGE 226
Db	124 GFRALRLHRVNVSSGVLKNFKDENGKFFCNFTGE-EGRGDKQVRSMLSLLRASEISFPGE 182
QY	227 KVMDEAETFSKYLREAL---QKIPASSILSLERDVLEYGWHTNLPRLRNMDVDFG 282
Db	183 KMEEAKAFTREYLNQVLAGHDVTDVDSQLLREVKYALEFPWHCVSRWEARSFLEIYG 242
QY	283 QHTK--NKNAAEKLLLELAKLEFNIFHSLQERELKHVSRWWKDSGSPMTFCRRHRHVEYYA 340
Db	243 HNHSWLKSNINQKMLKLAKLDFNILQCKHKEIQFITRWRDSGISQLNFYKRHRHVEYS 302
QY	341 LASCIAFEPQHSGERLGTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLP 400
Db	303 WVVMCIFEPFESERIAFAKTAICTVLDDLYDTHATLHEIKIMTEGVRRWDLSTLDDLP 362
QY	401 EYMGVYMMVYHTVNEMARVAEKAQGRDITLNYARQAWAEACFDSYMQEAKWIATGYLPTFE 460
Db	363 DYIKIAFQFFENTVNELIVEIVKRQGRDMTTIVKDCWKRYIESYQLQEAEMIATGHIPTFN 422
QY	461 EYLENGKVSSAHRPCALQPILTDIPFPDHILKEVDFFPSKLNLDLICIILRLRGDTRCYKA 520
Db	423 EYKNGMASSGMCIILNPLLLDKLLPDNILEQIHSPSKILDLELTGRIADDLKDFED 482
QY	521 DRARGEAEASSISCYMKDNPGLTEEDALNHINFMIRDARELNWELLKPDNSVPITSKKHA 580
Db	483 EKERGEMASSLQCYMKENPESTVENALNHKILNRSLEEFNWEFMKQD-SVPMCKCKFT 541
QY	581 FDISRVVWHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
Db	542 FNIGRGLQFIYKYRDGLYISDKEVKDQIFKILVHQVPM 579

Search completed: July 7, 2004, 17:43:43  
Job time : 48 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:41:07 ; Search time 52 Seconds  
(without alignments)  
3699.488 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRCLSSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3251	100.0	618	14	US-10-025-145A-65 Sequence 65, Appl
2	2453	75.5	628	9	US-09-887-586A-20 Sequence 20, Appl
3	2453	75.5	628	9	US-09-903-012-20 Sequence 20, Appl
4	2453	75.5	628	10	US-09-900-797-20 Sequence 20, Appl
5	2453	75.5	628	12	US-09-893-820-20 Sequence 20, Appl
6	2453	75.5	628	13	US-10-041-007-22 Sequence 22, Appl
7	2453	75.5	628	14	US-10-025-145A-4 Sequence 4, Appli
8	2264	69.6	630	14	US-10-025-145A-67 Sequence 67, Appl
9	2200.5	67.7	627	9	US-09-887-586A-30 Sequence 30, Appl
10	2200.5	67.7	627	9	US-09-903-012-30 Sequence 30, Appl
11	2200.5	67.7	627	10	US-09-900-797-30 Sequence 30, Appl
12	2200.5	67.7	627	12	US-09-893-820-30 Sequence 30, Appl
13	2200.5	67.7	627	13	US-10-041-007-26 Sequence 26, Appl
14	2200.5	67.7	627	14	US-10-025-145A-2 Sequence 2, Appli
15	2197.5	67.6	627	14	US-10-025-145A-32 Sequence 32, Appl

16	2137	65.7	630	14	US-10-025-145A-78	Sequence 78, Appl
17	2084.5	64.1	637	13	US-10-041-007-28	Sequence 28, Appl
18	2084.5	64.1	637	14	US-10-025-145A-69	Sequence 69, Appl
19	2031.5	62.5	637	9	US-09-887-586A-58	Sequence 58, Appl
20	2031.5	62.5	637	9	US-09-903-012-58	Sequence 58, Appl
21	2031.5	62.5	637	10	US-09-900-797-58	Sequence 58, Appl
22	2031.5	62.5	637	12	US-09-893-820-58	Sequence 58, Appl
23	2031.5	62.5	637	13	US-10-041-007-24	Sequence 24, Appl
24	2031.5	62.5	637	14	US-10-025-145A-6	Sequence 6, Appli
25	1295.5	39.8	581	9	US-09-887-586A-48	Sequence 48, Appl
26	1295.5	39.8	581	9	US-09-903-012-48	Sequence 48, Appl
27	1295.5	39.8	581	10	US-09-900-797-48	Sequence 48, Appl
28	1295.5	39.8	581	12	US-09-893-820-48	Sequence 48, Appl
29	1295.5	39.8	581	13	US-10-041-007-18	Sequence 18, Appl
30	1250.5	38.5	577	14	US-10-025-145A-18	Sequence 18, Appl
31	1240.5	38.2	862	9	US-09-887-586A-44	Sequence 44, Appl
32	1240.5	38.2	862	9	US-09-903-012-44	Sequence 44, Appl
33	1240.5	38.2	862	10	US-09-900-797-44	Sequence 44, Appl
34	1240.5	38.2	862	12	US-09-893-820-44	Sequence 44, Appl
35	1240.5	38.2	862	12	US-10-041-018-386	Sequence 386, App
36	1240.5	38.2	862	13	US-10-041-007-41	Sequence 41, Appl
37	1231	37.9	593	9	US-09-887-586A-50	Sequence 50, Appl
38	1231	37.9	593	9	US-09-903-012-50	Sequence 50, Appl
39	1231	37.9	593	10	US-09-900-797-50	Sequence 50, Appl
40	1231	37.9	593	12	US-09-893-820-50	Sequence 20, Appl
41	1231	37.9	593	13	US-10-041-007-20	Sequence 20, Appl
42	1187	36.5	782	9	US-09-887-586A-46	Sequence 46, Appl
43	1187	36.5	782	9	US-09-903-012-46	Sequence 46, Appl
44	1187	36.5	782	10	US-09-900-797-46	Sequence 46, Appl
45	1187	36.5	782	12	US-09-893-820-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1  
US-10-025-145A-65  
; Sequence 65, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR18414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 618  
; TYPE: PRT  
; ORGANISM: Abies Grandis  
US-10-025-145A-65

Query Match 100.0%; Score 3251; DB 14; Length 618;  
Best Local Similarity 100.0%; Pred. No. 1.4e-302;  
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 LVDDVERLGIDRHFKEIKTALDYVNSYWNKEGICGGRSVVTDLNSTALGLRTLRLHGY 180  
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Db 181 TVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGKVMDEAETFTSKYL 240  
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Db 241 REALQKIPASSILSLERDVLEYGWHTNLPRLRNMYMDVFGQHTKNKNAEKLLELAKL 300  
QY 301 EFNIFHSLQERELKHVSRRWKDSGSPMTFCRHRHVEYYALASCIAPFQHSGLGFTK 360  
Db 301 EFNIFHSLQERELKHVSRRWKDSGSPMTFCRHRHVEYYALASCIAPFQHSGLGFTK 360  
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Db 361 MSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVYMMVYHTVNEMARV 420  
QY 421 AEKAQGRDTLNYARQAWAEACFDSYMQEAKWIATGYLPTFEEYLENGKVSSAHRPCALQPI 480  
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QY 481 LTLDIPFPDHILKEVDPPSKLNDLICIILRLRGDTRCYKADRARGEESYSCYMKDNPG 540  
Db 481 LTLDIPFPDHILKEVDPPSKLNDLICIILRLRGDTRCYKADRARGEESYSCYMKDNPG 540  
QY 541 LTEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVVHHGYRYRDGYSFA 600  
Db 541 LTEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVVHHGYRYRDGYSFA 600  
QY 601 NVETKSLVMRTVIEPVPL 618  
Db 601 NVETKSLVMRTVIEPVPL 618

RESULT 2  
US-09-887-586A-20  
; Sequence 20, Application US/09887586A  
; Patent No. US20020094556A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094556A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/887,586A  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 628  
; TYPE: PRT  
; ORGANISM: Abies grandis  
US-09-887-586A-20

Query Match 75.5%; Score 2453; DB 9; Length 628;  
Best Local Similarity 75.3%; Pred. No. 5.9e-226;  
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;  
QY 1 MALLSITPLVRSCL-----SSSHEIKALRRITPTLGICRPGKSVAHSNMCLTSVASTD 55  
Db 1 MALVSTAPLASKCLHKSLSSTHELKALSRTIPALGMSRRGKSGITPSISMSSTTVVTTDD 60

QY 56 SVQRRVGNHNSLWDDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGG--- 112  
Db 61 GVRRRMGDFHNSLWDDDDVIQSL-PTAYEEKSYLERAELKIGEVKN-MFNSMSLEDGELMS 118  
QY 113 --NDLLQRLLLVDDVERLGIDRHFKEIKTALDYVNSYWNKEGICGGRSVVTDLNSTAL 170  
Db 119 PLNDLIQRLWIVDSLRLGIHRHFKEIKSALDYVYSYWGENGICGGRSVVTDLNSTAL 178  
QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGKVM 230  
Db 179 GLRTLRLHGYPVSSDVPKAFKQNGQFSCSENIQTDEEIRGVNLFRASLVAFPGKIMD 238  
QY 231 EAETFTSKYLREALQKIPASSILSLERDVLEYGWHTNLPRLRNMYMDVFGQHTKNKNA 290  
Db 239 EAEIFSTKYLKEALQKIPVSS-LSREIGDVLEYGWHTYLPRLARNYIQVFGQDTENTKS 297  
QY 291 --AEKLLLELAKLEFNIFHSLQERELKHVSRRWKDSGSPMTFCRHRHVEYYALASCI 347  
Db 298 YVKSCKLLELAKLEFNIFQSLQKRELESVRRWKESGFPMTFCRHRHVEYYTLASCI 357  
QY 348 EPQHSGLRGLFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407  
Db 358 EPQHSGLRGLFAKTCHLITVLDMDYDVGTVDELELFTATMKRWDPSIDCLPEYMKGVY 417  
QY 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAWAEACFDSYMQEAKWIATGYLPTFEEYLENGK 467  
Db 418 IAVYDTVNEMAREAEAAQGRDTLTLYAREAWAVIDSYMQEARWIATGYLPSFDEYYENGK 477  
QY 468 VSSAHRPCALQPILTLDIPFPDHILKEVDPPSKLNDLICIILRLRGDTRCYKADRAGEE 527  
Db 478 VSCGHRISALQPILTMDIPFPDHILKEVDPPSKLNDLACAILRLRGDTRCYKADRAGEE 537  
QY 528 ASSISCYMKDNPLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVW 587  
Db 538 ASSISCYMKDNPGVSEEDALDHINAMISDVIKLNWELLKPDINVPISAKKHAFDIARAF 597  
QY 588 HHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618  
Db 598 HYGKYRDGYSVANVETKSLVTRTLLESVPL 628

RESULT 3  
US-09-903-012-20  
; Sequence 20, Application US/09903012  
; Patent No. US20020094557A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094557A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/903,012  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,993  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 628  
; TYPE: PRT  
; ORGANISM: Abies grandis  
US-09-903-012-20

Query Match 75.5%; Score 2453; DB 9; Length 628;  
Best Local Similarity 75.3%; Pred. No. 5.9e-226;  
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;





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; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-893-820-20

Query Match      75.5%; Score 2453; DB 12; Length 628;
Best Local Similarity 75.3%; Pred. No. 5.9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

QY 1 MALLSITPLVSRSL-----SSSHEIKALRRRTIPTLGICRPGKSVAHNSINMCLTSVASTD 55
   |||:| || | ||| |||:| ||| ||| |||:| ||| ||| |||:| ||| ||| |||:|
Db 1 MALVSTAPLASKSCLHKSLISSTHELKALSRTIPALGMSRRGKSITPSSISMSSTTVVTTDD 60
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 56 SVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGG--- 112
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GVRRRMGDFHNSLWDDDDVIQSL-PTAYEEKSYLERAEKLIGEVKN-MFNSMSLEDGELMS 118
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 113 --NDLLQRLLLVDDVERLGIDRHFKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 PLNDLIQRLWIVDSLRLGIHRHFKEIKSALDYVYSYWGNGIGCGRESVVTDLNSTAL 178
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLNFRASLVAFPGEKVM 230
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLNFRASLVAFPGEKIM 238
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 231 EAETFTSKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLARNYMDVFGQHTKNKNA 290
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 EAEIFSTKYLKEALQKIPVSS-LSREIGDVLEYGWHTYLPRLARNYIQVFGQDTENTKS 297
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 291 ---AEKLELAKLEFNIFHSLQERELKHVSRRWKDSGSPMTFCRHRHVEYYALASCI 347
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 YVKSCKLLELAKLEFNIFQSLQKRELESVLRWVKESGFPEMTFCRHRHVEYYTLASCI 357
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 348 EPQHSGFRLGFTKMSHLITVLDMDYDVFGTVDELELFTATIKRWDPSPAMECLPEYMKGV 407
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 EPQHSGFRLGFAKTCHLITVLDMDYDTFGTVDELELFTATMKRWDPSIDCLPEYMKGV 417
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAEACFDSYMQEAKWIATGYLPTFEEYLENGK 467
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 IAVYDTVNEMAREAEAAQGRDTLTLYAREAEAYIDSYMQEARWIAATGYLPSFDEYYENG 477
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 468 VSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNLDLCIILRLRGDTRCYKADRAGEE 527
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 VSCGHRISALQPILTMDIPFPDHILKEVDFPSKLNLDLACAILRLRGDTRCYKADRAGEE 537
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVW 587
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 ASSISCYMKDNPVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKKHAFDIARAF 597
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 588 HGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 HGYKYRDGYSVANVETKSLVTRTLLESVPL 628
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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RESULT 6
US-10-041-007-22
; Sequence 22, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthese
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
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US-10-041-007-22

Query Match      75.5%; Score 2453; DB 13; Length 628;
Best Local Similarity 75.3%; Pred. No. 5.9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

QY 1 MALLSITPLVSRSL-----SSSHEIKALRRRTIPTLGICRPGKSVAHNSINMCLTSVASTD 55
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MALVSTAPLASKSCLHKSLISSTHELKALSRTIPALGMSRRGKSITPSSISMSSTTVVTTDD 60
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 56 SVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGG--- 112
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GVRRRMGDFHNSLWDDDDVIQSL-PTAYEEKSYLERAEKLIGEVKN-MFNSMSLEDGELMS 118
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 113 --NDLLQRLLLVDDVERLGIDRHFKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 PLNDLIQRLWIVDSLRLGIHRHFKEIKSALDYVYSYWGNGIGCGRESVVTDLNSTAL 178
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLNFRASLVAFPGEKVM 230
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLNFRASLVAFPGEKIM 238
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 231 EAETFTSKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLARNYMDVFGQHTKNKNA 290
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 EAEIFSTKYLKEALQKIPVSS-LSREIGDVLEYGWHTYLPRLARNYIQVFGQDTENTKS 297
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 291 ---AEKLELAKLEFNIFHSLQERELKHVSRRWKDSGSPMTFCRHRHVEYYALASCI 347
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 YVKSCKLLELAKLEFNIFQSLQKRELESVLRWVKESGFPEMTFCRHRHVEYYTLASCI 357
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 348 EPQHSGFRLGFTKMSHLITVLDMDYDVFGTVDELELFTATIKRWDPSPAMECLPEYMKGV 407
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 EPQHSGFRLGFAKTCHLITVLDMDYDTFGTVDELELFTATMKRWDPSIDCLPEYMKGV 417
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAEACFDSYMQEAKWIATGYLPTFEEYLENGK 467
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 IAVYDTVNEMAREAEAAQGRDTLTLYAREAEAYIDSYMQEARWIAATGYLPSFDEYYENG 477
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 468 VSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNLDLCIILRLRGDTRCYKADRAGEE 527
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 VSCGHRISALQPILTMDIPFPDHILKEVDFPSKLNLDLACAILRLRGDTRCYKADRAGEE 537
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVW 587
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 ASSISCYMKDNPVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKKHAFDIARAF 597
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 588 HGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 HGYKYRDGYSVANVETKSLVTRTLLESVPL 628
   |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 7
US-10-025-145A-4
; Sequence 4, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
```

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; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies Grandis
US-10-025-145A-4

Query Match      75.5%; Score 2453; DB 14; Length 628;
Best Local Similarity 75.3%; Pred. No. 5.9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

Qy 1 MALLSITPLVSRSL-----SSSHEIKALRRRTIPTLGICRPGKSVAH SINMCLTSVASTD 55
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 1 MALVSTAPLASKSLHKSLISSTHELKALSRITPALGMSRRGKSI TPSISMSSTTVVTTDD 60

Qy 56 SVQRRVGNHNSNLWDDDFIQSLISTPYGADPYRERADRRLIGEVDIMFNFKSLEDGG--- 112
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 61 GVRRRMGDFHNSNLWDDDFIQSL-PTAYEEKSYLERAELKIGEVKN-MFNMSLEDGELMS 118

Qy 113 --NDLLQRLLLVDDVERLIGDRHFKEIKTALDYVNSYWNKGGICGRESVVTDLNSTAL 170
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 119 PLNDLIQRLWI VDSLRLGIHRHFKEIKSALDYVYSYWGENGICGRESVVTDLNSTAL 178

Qy 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 230
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 179 GLRTLRLHGYTVSSDVFKA FKQGQNGQFSCSENIQTDEEIRGVNLFRASLIAFPGEKIM 238

Qy 231 EAETFSTKYLRREALQKIPASSILSLEIRDVLEYGWHTNLPRLRLEARNYMDVFGQHTKN 290
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 239 EAEIFSTKYLRREALQKIPVSS-LSREIGDVLGYGWHTYLPRLRLEARNYIQVFGQDTENT 297

Qy 291 ---AEKLELAKLEFNIFHSLQERELKHVSRWWKDSGSPMTFCRHRHVEYYALASCI 347
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 298 YVKSCKLLELAKLEFNIFQSLQKRELESVLRWWKESGFPEMTFCRHRHVEYYTLASCI 357

Qy 348 EPQHSGRFGFTKMSHLITVLDMDYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 358 EPQHSGRFGFTKMSHLITVLDMDYDTFGTVDELELFTATMKRWDPSIDCLPEYMKGVY 417

Qy 408 MMVYHTVNMARVAEKAQGRDTLNYARQAWACFDSYMQEAKWIATGYLPTFEEYLENGK 467
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 418 IAVYDTVNMAREAEAAQGRDTLT YAREAWAYIDSYMQEARWIATGYLPSFDEYYENGK 477

Qy 468 VSSAHRPCALQPI LTLDIPFPDHILKEVDPSKNDLICIILRLRGDTRCYKADRAGEE 527
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 478 VSCGHRISALQPI LTMDIPFPDHILKEVDPSKNDLACAILRLRGDTRCYKADRAGEE 537

Qy 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRV 587
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 538 ASSISCYMKDNPGVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKKHAFDIARAF 597

Qy 588 HHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 598 HYGKYRDGYSVANVETKSLVTRTLLESVPL 628

RESULT 8
US-10-025-145A-67
; Sequence 67, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
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; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Abies Grandis
US-10-025-145A-67

Query Match      69.6%; Score 2264; DB 14; Length 630;
Best Local Similarity 68.3%; Pred. No. 8.2e-208;
Matches 435; Conservative 78; Mismatches 98; Indels 26; Gaps 9;

Qy 1 MALLSITPLVSRSL-----SSSHEIKALRRRTIPTLGICRPGKSVAH SINMCLTSVAST 54
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 1 MALVSSAP---KSLHKSLIRSTHHELKPLRRTIPTLGCMCRRGKSFTPSVMSLTAVSD 57

Qy 55 DSVQRRVGNHNSNLWDDDFIQSLISTPYGADPYRERADRRLIGEVDIMFNFKSLEDGG-- 112
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 58 DGLQRRIGDYHNSNLWDDDFIQSL-STPYGEPSYRERAELKIGEVKE-MFNSMPSEDEGSM 115

Qy 113 --NDLLQRLLLVDDVERLIGDRHFKEIKTALDYVNSYWNKGGICGRESVVTDLNSTA 169
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 116 SPLNDLIERLWMVDSVERLIGDRHFKEIKSALDYVYSYWNKGGICGGRDSVFPDVNSTA 175

Qy 170 LGLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 229
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 176 SGFRTLRLHGYSVSSEVLKVFDQNGQFAPSPSTK-ERDRTVLNLFRASFIAPFGEKVM 234

Qy 230 DEAEFTSTKYLRREALQKIPASSILSLEIRDVLEYGWHTNLPRLRLEARNYMDVFGQHT--- 285
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 235 EAEIFSSRYLKEAVQKIPVSS-LSQEIDYLTLEYGWHTNMPRLTRNLDVFGHPTSPWL 293

Qy 286 KNKNA---AEKLELAKLEFNIFHSLQERELKHVSRWWKDSGSPMTFCRHRHVEYYAL 341
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 294 KKKRTQYLDSEKLELAKLEFNIFHSLQEKELQYLSRWIHSGLPELTFGRHRHVEYYTL 353

Qy 342 ASCIAFEPQHSGRFGFTKMSHLITVLDMDYDVFGTVDELELFTATIKRWDPSAMECLPE 401
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 354 SSCIAFEPKHSARLGFAGTCHLITVLDMDIYDTFTGMTDEIELFNEAVRRWNPSEKERLPE 413

Qy 402 YMKGVYMMVYHTVNMARVAEKAQGRDTLNYARQAWACFDSYMQEAKWIATGYLPTFEE 461
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 414 YMKEIYMALYEAALTMAREAEKTQGRDTLNYARKAWEVYLDSTYQEAKEWIASGYLPTFEE 473

Qy 462 YLENGKVSSAHRPCALQPI LTLDIPFPDHILKEVDPSKNDLICIILRLRGDTRCYKAD 521
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 474 YLENAKVSSGHRAAALTPLLTLDVPLPDDVLKIDFPSPRFNDLASSFLRLRGDTRCYKAD 533

Qy 522 RARGEAEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAF 581
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 534 RDRGEEASSISCYMKDNPGLTEEDALNHINAMINDI IKELNWELLKPDNSNIPMTARKHAY 593

Qy 582 DISRVVHHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
   |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 594 EITRAFHQLYKYRDGFSVATQETKSLVTRTVLEPVPL 630

RESULT 9
US-09-887-586A-30
; Sequence 30, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
```





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; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-900-797-30

Query Match      67.7%; Score 2200.5; DB 10; Length 627;
Best Local Similarity 68.1%; Pred. No. le-201;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY      1 MALLSITPLVSRSL-----SSSHEIKALRRRTIPTLGICRPGKSVAH SINCLTSVASTD 55
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      1 MALVSIPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRGRGKSVTPSMSISLATAAPDD 60
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      56 SVQRRVGNVHSNLWDDDFIQSLISTPYGAPDYRERADRLLIGEVKDIMFNFKSLEDGG--- 112
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPYQYERAEERLIVEVKKI-FNSMYLDDGRLMS 118
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      113 --NDLQRLLLVDDVERLGLIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      119 SFNDLMQRLWIVDSVERLGIARHFKEIITSALDYVPFYWEENGIGCGRDSIVTDLNSTAL 178
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      171 GLRTRLRHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGEKVMD 230
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      179 GERTLRHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYRASLIAFPGEKVME 237
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      231 EAETFTSKYLREALQKIPASSILSLFIRDVLEYGWHTNLPRLERNYMDVFGQHTK---N 287
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYEGWHTNLPRLERNYIDTLEKDTSAWLN 296
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      288 KNAEKLLELAKLEFNFHLSQERELKHVSRWWDKSGSPMTFCRHRHVEYYALASCI AF 347
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      297 KNAGKLLLELAKLEFNFNSLQOKELQYLLRWKKESDLPKLTFAHRHVEFYTLASCI AI 356
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      348 EPQHSGRFLGFTKMSHLITVLDDMYDVFGTVDELELTATIKRWDPSPAMECLPEYMKGVY 407
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      357 DPKHSAFRLGFAKMCHLVTVLDDIYDTFGTIDELELFTSAIKRWNSSEIEHLPEYMKCVY 416
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      408 MMVYHTVNEMARVAEKAQGRDRTLNYARQAWAEACFDSYMOEAKWIATGYLPTFEEYLENGK 467
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      417 MVVFEITVNELTREAEKTQGRNTLNYVRKAWAEAYFDSYMEEAKWISNGYLPMEFEYHENGK 476
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      468 VSSAHRPCALQPILTDIPFPDHILKEVDFPSKLNLDLICIILRLRGDTRCYKADRARGE 527
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      477 VSSAYRVATLQPILTNLAWLPDYILKGIDFPFRFNDLASSFLRLRGDTRCYKADRDRGEE 536
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      528 ASSISCYMKDNPGLTEEDALNHINFMIRDIAIRELNWELLKPDNSVPITSKKHAFDISRVW 587
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      537 ASCISCYMKDNPGSTEEEDALNHINAMVNDI IKELNWELLRSNDNIPMLAKKHAFDITRAL 596
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

QY      588 HHGYRYRDGYSFANVETKSLVMRTVIE 614
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||
Db      597 HHLYIYRDGFSVANKETKKLVMETLLE 623
      |||:|||||:||||| |||:|||||:||||| |||:|||||:||||| |||:|||||:|||||

RESULT 12
US-09-893-820-30
; Sequence 30, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-893-820-30

Query Match      67.7%; Score 2200.5; DB 12; Length 627;
Best Local Similarity 68.1%; Pred. No. 1e-201;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

Qy      1 MALLSITPLVRSCL-----SSSHEIKALRRTIPTLGICRPGKSVAHSINCLTSSVASTD 55
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      1 MALVSISPLASKSLCRKSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60

Qy      56 SVQRRVGNVHSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGG-- 112
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPYQERAERLIVEVKKI-FNSMYLDDGRLMS 118

Qy      113 --NDLLQRLLLVDDVERLIGDRHFKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      119 SFNDLMQRLWIVDSVERLGIARHFKEITSAIDYVFRYWEENGIGCGRDSIVTDLNSTAL 178

Qy      171 GLRTLRLHGYTVSSDDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVMD 230
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      179 GFRTLRLHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYRASLIAFPGEKVME 237

Qy      231 EAETESTKYLREALQKIPASSILSLEIRDVLEYGWHWTNLPRLRARNYMDVFGQHTK---N 287
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGWHTNLPRLRARNYIDTLEKDTSAWLN 296

Qy      288 KNAEKLLELAKLEFNIFHSLQERELKHVSRKWKDSCGSPMTFCRHRHVEYYALASCIAP 347
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      297 KNAGKKLLELAKLEFNIFNSLQQLQELQYLLEWVKESDLPKLTTFARHRHVEFYTLASCI 356

Qy      348 EPQHSGRFLGFTKMSHLITVLDDMYDVFVDELELFTATIKRWDPSAMECLPEYMKGVY 407
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      357 DPKHSAFRLGFAKMCHLVTVLDDIYDTFGTIDELELFTSAIKRWNSSIEIHLPEYMKCVY 416

Qy      408 MMVYHTVEMARVAEKAQGRDRTLNYARQAWAEACFDSYMQEAQKWIATGYLPTFEEYLENGK 467
      |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      417 MVVFETVNELTREAEKTQGRNTLNVYRKAWAEAYFDSYMEEAKWISNGYLPMEFEEYHENGK 476

Qy      468 VSSAHRPCALQPILTLDIPFPDHILKEVDFFPSKLNLDLICIILRLRGDTRCYKADRAGEE 527
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      477 VSSAYRVATLQPILTNLAWLPDYILKGIDFSPRFNDLASSFLRLRGDTRCYKADRAGEE 536

Qy      528 ASSISCYMKDNPGLTEEDALNHINFMIRDARELNWELLKPDNSVPITSKKHAFDISRVW 587
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      537 ASCISCYMKDNPGSTEEADLNHINAMVNDIikelNWELLRSNDNIPMLAKKHAFDITRAL 596

Qy      588 HHGYRYRDGYSFANVETKSLVMRTVIE 614
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      597 HHLYIYRDGFSVANKETKKLVMTLLE 623
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 12  
US-09-893-820-30  
; Sequence 30, Application US/09893820  
; Publication No. US20040053386A1  
; GENERAL INFORMATION:



RESULT 15  
US-10-025-145A-32  
; Sequence 32, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Abies Grandis  
US-10-025-145A-32

Query Match 67.6%; Score 2197.5; DB 14; Length 627;  
Best Local Similarity 68.1%; Pred. No. 2e-201;  
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY	1	MALLSITPLVSRSL-----SSSHEIKALRRTIPTLGICRPGKSVAH SINMCLTSVASTD	55
Db	1	MALVSIISPLASKSLRKSLSISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD	60
QY	56	SVQRRVGNVHSLWDDDFIQSLISTPYGADPYRERADRLIGEVKDIMFNPKSLEDGG---	112
Db	61	GVQRRIGDYHSLWDDDFIQSL-SHYGEPSTYQERAERLIVEVKI-FNSMYLDDGR LMS	118
QY	113	--NDLLQRLLLVDDVERLGIDRHFKEIKTALDYVNSYNWKEGICGGRSVVTDLNSTAL	170
Db	119	SFNDLMQRLWIVDSVERLGIARHFKEITSALDYVFRYWEENGICGGRDSIVTDLNSTAL	178
QY	171	GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLNFRASLVAFPGEK VMD	230
Db	179	GFRTLRLHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVLNLRYASLIAFPGEK VME	237
QY	231	EAETFTSKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRL EARNYMDVFGQHTK---N	287
Db	238	EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGWHTNLPRL EARNYIDTLEKDOTSAWL N	296
QY	288	KNAAEKLELAKLEFNIFHSLQERELKHVSRWKDSCGSPMTFCRHRHVEYYALASCI AF	347
Db	297	KNAGKKLELAKLEFNIFNSLQKELQYLLRWKESDLPKLTFA RHRHVEFYTLASCI AI	356
QY	348	EPQHSGRFLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGV Y	407
Db	357	DPKHSAFRLGFAKMHVTLVLDIYDTFGTIDELELFTSAIKR WNSSEIEHLPYMKCVY	416
QY	408	MMVYHTVNEMARVAEKAQGRDTLNYARQAWAECFDSYMQE AKWIATGYLPTFEEYLENGK	467
Db	417	MVVFETVNELTREAEKTQGRNTLNVYRKAWAEAYFDSYMEE AKWISNGYLPFEEYHENGK	476
QY	468	VSSAHRPCALQPILTLDIPFPDHILKEVDFPFSKLN DLICIIILRLRGDTRCYKADRGE E	527
Db	477	VSSAYRVATLQPILTNLAWLPDYILKGIDFPSPFN DLASSFLRLRGDTRCYKADRDRGE E	536
QY	528	ASSISCYMKONPGLTEEDALNHINFMIRDAIRELNWELLKPD NSVPITSKKHAFDISRVW	587
Db	537	ASCISCYMKONPGTEEDALNHINAMVNDIIKELNWELLRSND NIPMLAKKHAFDITRAL	596
QY	588	HGGRYRDGYSFANVETKSLVMRTVIE	614

Db 597 HHLYIYRDGFSVANKETKKLVMETLLE 623  
Search completed: July 7, 2004, 17:45:19  
Job time : 53 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 8, 2004, 12:35:55 ; Search time 6774 Seconds  
(without alignments)  
3954.236 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRCLSSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10025145/runat\_07072004\_160149\_27936/app\_query.fasta\_1.775  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10025145@cgn\_1\_1\_4198 @runat\_07072004\_160149\_27936 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3251	100.0	2013	6	AR222136	AR222136 Sequence
2	3251	100.0	2013	8	AGU87910	U87910 Abies grand
3	2456.5	75.6	1958	8	AY237645	AY237645 Picea sit
4	2453	75.5	2018	6	BD2227661	BD2227661 Synthases
5	2453	75.5	2018	6	AR222097	AR222097 Sequence
6	2453	75.5	2018	6	AR240696	AR240696 Sequence
7	2453	75.5	2018	6	AR266971	AR266971 Sequence
8	2453	75.5	2018	6	AR316320	AR316320 Sequence
9	2453	75.5	2018	6	AR338463	AR338463 Sequence
10	2453	75.5	2018	6	AR429869	AR429869 Sequence
11	2453	75.5	2018	8	AGU87909	U87909 Abies grand
12	2328.5	71.6	2082	8	AF543527	AF543527 Pinus tae
13	2266.5	69.7	2162	8	AF543529	AF543529 Pinus tae
14	2264	69.6	2186	6	AR222137	AR222137 Sequence
15	2264	69.6	2186	8	AF139205	Abies gra
16	2237	68.8	2198	8	AF369918	AF369918 Picea abi
17	2205.5	67.8	2150	8	AF369919	AF369919 Picea abi
18	2200.5	67.7	2196	6	BD227666	BD227666 Synthases
19	2200.5	67.7	2196	6	AR222096	AR222096 Sequence
20	2200.5	67.7	2196	6	AR240701	AR240701 Sequence
21	2200.5	67.7	2196	6	AR266976	AR266976 Sequence
22	2200.5	67.7	2196	6	AR316325	AR316325 Sequence
23	2200.5	67.7	2196	6	AR338468	AR338468 Sequence
24	2200.5	67.7	2196	6	AR429874	AR429874 Sequence
25	2200.5	67.7	2196	8	AGU87908	U87908 Abies grand
26	2197.5	67.6	2205	6	AR222116	AR222116 Sequence
27	2163.5	66.5	2186	8	AF461460	AF461460 Picea abi
28	2151	66.2	2100	8	AF543530	AF543530 Pinus tae
29	2137	65.7	1890	6	AR222146	AR222146 Sequence
30	2137	65.7	1893	8	AF139206	AF139206 Abies gra
31	2084.5	64.1	2429	6	AR222138	AR222138 Sequence
32	2084.5	64.1	2429	8	AF139207	AF139207 Abies gra
33	2046.5	62.9	3306	8	AF326517	AF326517 Synthases
34	2031.5	62.5	2089	6	BD227677	BD227677 Synthases
35	2031.5	62.5	2089	6	AR222098	AR222098 Sequence
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37	2031.5	62.5	2089	6	AR266987	AR266987 Sequence
38	2031.5	62.5	2089	6	AR316336	AR316336 Sequence
39	2031.5	62.5	2089	6	AR338479	AR338479 Sequence
40	2031.5	62.5	2089	6	AR429885	AR429885 Sequence
41	2031.5	62.5	2089	8	AF006193	AF006193 Abies gra
42	1985.5	61.1	1960	8	AF543531	AF543531 Pinus tae
43	1921.5	59.1	2084	8	AF543528	AF543528 Pinus tae
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ALIGNMENTS

AR222136  
LOCUS AR222136 2013 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 64 from patent US 6429014.  
ACCESSION AR222136  
VERSION AR222136.1 GI:23329510  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 2013)  
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.  
TITLE Monoterpene synthases from grand fir (*Abies grandis*)  
JOURNAL Patent: US 6429014-A 64 06-AUG-2002;  
FEATURES  
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Score: 3251.00 Matches: 618  
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LOCUS	AGU87910	2013 bp	mrna linear
DEFINITION	Abies grandis (-)-camphene synthase (AG6.5)	mrna	PLN 10-AUG-2001
ACCESSION	U87910		complete cds.
VERSION	U87910.1	GI:2411484	
KEYWORDS			
SOURCE			
ORGANISM	Abies grandis		
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	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.		
REFERENCE	1	(bases 1 to 2013)	
AUTHORS	Bohlmann,J., Steele,C.L. and Croteau,R.		
TITLE	Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase		
JOURNAL	J. Biol. Chem.	272 (35), 21784-21792	(1997)
MEDLINE	97413772		
PUBMED	9268308		
REFERENCE	2	(bases 1 to 2013)	
AUTHORS	Bohlmann,J., Phillips,M., Ramachandiran,V., Katoh,S. and Croteau,R.		
TITLE	cDNA cloning, characterization, and functional expression of four new monoterpene synthase members of the Tpsd gene family from grand fir (Abies grandis)		
JOURNAL	Arch. Biochem. Biophys.	368 (2), 232-243	(1999)
MEDLINE	99373092		
PUBMED	10441373		
REFERENCE	3	(bases 1 to 2013)	
AUTHORS	Bohlmann,J., Steele,C.L. and Croteau,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-JAN-1997)	Institute of Biological Chemistry, Washington State University, Clark Hall, Pullman, WA 99164-6340,	
USA			
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Score:	3251.00	Matches:	618
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00%		Mismatches: 0	
Query Match: 100.00%		Indels: 0	
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QY	121	LeuValAspAspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThr	140
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QY	141	AlaLeuAspTyrValAsnSerTyrTrpAsnGluLysGlyIleGlyCysGlyArgGluSer	160
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QY	161	ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr	180
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QY	321	LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla	340
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LOCUS AY237645 1958 bp mRNA linear PLN 13-SEP-2003  
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ACCESSION AY237645  
VERSION AY237645.1 GI:34582666  
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ORGANISM Picea sitchensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
REFERENCE 1 (bases 1 to 1958)  
AUTHORS Byun McKay, S.A., Hunter, W.L., Godard, K.A., Wang, S.X., Martin, D.M.,  
Bohlmann, J. and Plant, A.L.  
TITLE Insect Attack and Wounding Induce Traumatic Resin Duct Development  
and Gene Expression of (-)-Pinene Synthase in Sitka Spruce

JOURNAL Plant Physiol. 133 (1), 368-378 (2003)  
PUBMED 12970502  
REFERENCE 2 (bases 1 to 1958)  
AUTHORS Byun McKay, A.S., Hunter, W.L., Goddard, K.A., Wang, S.X., Martin, D.,  
Bohlmann, J. and Plant, A.L.  
TITLE Direct Submission  
JOURNAL Submitted (17-FEB-2003) Biology, Simon Fraser University, 8888  
University Drive, Burnaby, BC V5A 1S6, Canada  
FEATURES  
Location/Qualifiers  
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1. .1958  
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ORIGIN

Alignment Scores: 1.17e-190 Length: 1958  
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Best Local Similarity: 75.56% Indels: 17  
Query Match: 8 Gaps: 7  
DB: 7  
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Db 669 AAAGACCAAAATGGGCAGTTTGCATGCTCTCCGAGT--CAGACAGAGGAAGAGATCAGA 725  
  
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Db 726 AGCGTACTCAATTATATCGGGCTTCCCTCATCGCCTTCCCGGGGAGAAAGTTATGGAA 785  
  
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QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507

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RESULT 4

BD227661  
LOCUS BD227661 2018 bp DNA linear PAT 17-JUL-2003  
DEFINITION Syntheses.  
ACCESSION BD227661  
VERSION BD227661.1 GI:33037431  
KEYWORDS JP 2002526066-A/13.  
SOURCE Abies grandis  
ORGANISM Abies grandis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.  
REFERENCE 1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Syntheses  
JOURNAL Patent: JP 2002526066-A 13 20-AUG-2002;  
UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES  
COMMENT OS Abies grandis (giant fir)  
PN JP 2002526066-A/13  
PD 20-AUG-2002  
PF 17-SEP-1999 JP 2000574228  
PR 18-SEP-1998 US 60/100993,22-APR-1999 US 60/130628 PR  
23-AUG-1999 US 60/150262  
PI JOSEPH CHAPPELL, KATHLEEN R MANNA, JOSEPH P NOEL, COURTNEY M PI STARKS  
PC C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10,C12N9/12,  
PC C12Q1/25,G01N33/68//(C12N9/12,C12R1:91),(C12N9/12,C12R1:19),  
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FEATURES  
source

ORIGIN

Alignment Scores:

Pred. No.: 2.34e-190 Length: 2018  
Score: 2453.00 Matches: 475  
Percent Similarity: 84.63% Conservative: 59  
Best Local Similarity: 75.28% Mismatches: 81

Query Match:	75.45%	Indels:	16
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QY	368	LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr	387
Db	1137	CTTGACGATATGTACGACACCTTCGSCACAGTAGACGAGCTGGAACTCTTCACAGCGACA	1196
QY	388	IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr	407
Db	1197	ATGAAGAGATGGGATCCGTCCTCGATAGATTGCCTTCCAGAATATATGAAAGGAGTGATC	1256
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Db	1317	GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATTGATTGCTATATGCAAGAA	1376
QY	448	AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys	467
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QY	528	AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu	547
Db	1617	GCTTCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC	1676
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QY	588	HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu	607
Db	1797	CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG	1856
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DEFINITION	AR222097		
ACCESSION	AR222097.1	GI:23329471	
VERSION	Unknown.		
KEYWORDS	Unclassified.		
SOURCE	1 (bases 1 to 2018)		
ORGANISM	Steele,C.L., Bohlmann,J. and Croteau,R.B.		
REFERENCE	Monoterpene synthases from grand fir (Abies grandis)		
AUTHORS			
TITLE			

JOURNAL

Patent: US 6429014-A 3 06-AUG-2002;

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Location/Qualifiers

source

1. .2018

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:

2.34e-190

Length:

2018

Score:

2453.00

Matches:

475

Percent Similarity:

84.63%

Conservative:

59

Best Local Similarity:

75.28%

Mismatches:

81

Query Match:

75.45%

Indels:

16

DB:

6

Gaps:

6

US-10-025-145A-65 (1-618) x AR222097 (1-2018)

Qy

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15

Db

6

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Qy

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Db

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836

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Db	837	CGATTGGAAGCAAGGAATTACATCCAAGTCTTTGGACAGGACACTGAGAAACACGAAGTCA	896
Qy	291	-----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer	307
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Qy	308	LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu	327
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Qy	328	MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe	347
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Qy	388	IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr	407
Db	1197	ATGAAGAGATGGGATCCGTCTCGATAGATTGCCTTCCAGAAATATATGAAAGGAGTGTAC	1256
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Qy	428	AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu	447
Db	1317	GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTCGTATATGCAAGAA	1376
Qy	448	AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys	467
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Qy	468	ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProphe	487
Db	1437	GTTAGCTGTGTCATCGCATATCCGCATATGCAACCCATTCTGACAATGGACATCCCCCTTT	1496
Qy	488	ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle	507
Db	1497	CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCTTAACGACTTGGCATGTGCC	1556
Qy	508	IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu	527
Db	1557	ATCCTTCGATTACGAGGTGATACGCGGTGCTACAAGGCGGACAGGGCTCGTGGAGAAGAA	1616
Qy	528	AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu	547
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Db	1677	GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAAATTTGGGAACCTTCTCAA	1736
Qy	568	ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp	587
Db	1737	CCAGACATCAATGTTCCCATCTCGCGGAAAGAAACATGCTTTTGACATCGCCAGAGCTTTC	1796
Qy	588	HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu	607
Db	1797	CATTACGCTACAAATACCGAGACGGCTACAGCGTTGCCAACCTTGAAACGAAGAGTTTG	1856
Qy	608	ValMetArgThrValIleGluProValProLeu	618
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AR240696  
LOCUS AR240696 2018 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 19 from patent US 6468772.  
ACCESSION AR240696  
VERSION AR240696.1 GI:27285845  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2018)  
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.  
TITLE Methods of making modified polypeptides  
JOURNAL Patent: US 6468772-A 19 22-OCT-2002;  
FEATURES Location/Qualifiers  
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Alignment Scores:  
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Percent Similarity: 84.63% Conservative: 59  
Best Local Similarity: 75.28% Mismatches: 81  
Query Match: 75.45% Indels: 16  
DB: 6 Gaps: 6  
US-10-025-145A-65 (1-618) x AR240696 (1-2018)  
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
Db 6 ATGGCTCTAGTTCTACCGCACCGTTGGCTTCCAAATCATGCGCTGCACAAATCGTTGATC 65  
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAAATTCAGCTCTAGGAATGAGTAGG 125  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 126 CGAGGGAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACCGTTGTAACCGATGAT 185  
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75  
Db 186 GGTGTACGAAGACGCATGGCGGATTTCCATTCCAACCTCTGGGACGATGTCATACAG 245  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGCTGAGAAACTGATC 302  
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 303 GGGGAAGTAAAGAAC---ATGTTCAATTCGATGTCATTAGAAAGATGGAGAGTTAATGAGT 359  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeuGlyIle 130  
Db 360 CCGTCAATGATCTCATTCAACGCCCTTTGGATTGTCGACAGCCTTGAACGTTTGGGGATC 419  
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValasnSerTyrTrpAsn 150  
Db 420 CATAGACATTTCAAAGATGAGATAAAATCGCGCTTGATTATGTTTACAGTTATTGGGGC 479  
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 480 GAAATGGCATCGGATCGGGAGGAGAGTGTGTTACTGATCTGAACTCAACTGCGTTG 539  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 540 GGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTCAAAGCTTTC 599  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
Db 600 AAAGGCCAAAATGGCGAGTTTTCTCTGTCTGAAATAATTCAGACAGATGAAGAGATCAGA 659

QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 660 GCGGTTCTGAATTTATTCGGGGCCTCCCTCATTCCTGCTTCCAGGGGAGAAAATTATGGAT 719  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 720 GAGGCTGAAATCTTCTCTACCAATAATTAAAGAGAGCCCTGCAAAAGATTCCGGTCTCC 779  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270  
Db 780 AGT---CTTTCGGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTGCCG 836  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290  
Db 837 CGATTGGAAGCAAGGAATTACATCCAGTCTTTGGACAGGACACTGAGAACACGAAAGTCA 896  
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307  
Db 897 TATGTGAAGAGCAAAAACCTTTTAGAACTCGCAAAATTGGAGTTCAACATCTTTCAATCC 956  
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327  
Db 957 TTACAAAAGAGGGAGTTAGAAAGTCTGGTTCAGATGGTGGAAAGAAATCGGGTTCCTGAG 1016  
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
Db 1017 ATGACCTTCTGCCGACATCGTCACTGCGTGAATACTACACTTTGGCTTCTCTGCATTGCGTTC 1076  
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
Db 1077 GAGCCTCAACATTTCTGATTTCAGACTCGGCTTTGCCAAGACGCTGTGATCTTATCACGGTT 1136  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387  
Db 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACTTTTCACAGCGACA 1196  
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
Db 1197 ATGAAGAGATGGGATCCGTCTCGATAGATTGCCTTCCAGAAATATATGAAAGGAGTGATC 1256  
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427  
Db 1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCGAGAGGCTCAAGGCCGA 1316  
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447  
Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATTGATTGTTATATGCAAGAA 1376  
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
Db 1377 GCAAGGTGGATCGCCACTGGTTACCTGCGCTCCTTTGATGAGTACTACGAGAATGGGAA 1436  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487  
Db 1437 GTTAGCTGTGTCATCGCATATCCGCATTCGAACCCATTCTGACAATGGACATCCCCTTT 1496  
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
Db 1497 CCTGATCATATCTCAAGGAAGTTGACTTCCCATCAAAGCTTAACGACTTGGCATGTGCC 1556  
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527  
Db 1557 ATCCTTCGATTACGAGGTGATACCGGCTGCTACCAAGCGGACAGGCGTCGTGGAGAAGAA 1616  
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547  
Db 1617 GCTTCCTCTATATCATGTTATATGAAAGACAATCTCTGGAGTATCAGAGGAAGATGCTCTC 1676  
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567  
Db 1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAAATTGGGAACCTTCTCAA 1736  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587



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Db      1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1799
      Qy      588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
      Db      1797 CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGGAAGAGTTTG 1856

Qy      608 ValMetArgThrValIleGluProValProLeu 618
      Db      1857 GTCACGAGAACCCCTCCTTGAATCTGTGCCTTTG 1889

RESULT 7
AR2666971
LOCUS      AR2666971                2018 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 19 from patent US 6495354.
ACCESSION  AR2666971
VERSION    AR2666971.1  GI:29696426
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 2018)
AUTHORS   Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE     Syntheses
JOURNAL   Patent: US 6495354-A 19 17-DEC-2002;
FEATURES   Location/Qualifiers
            source          1..2018
                        /organism="unknown"
                        /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:      2.34e-190      Length:      2018
Score:          2453.00      Matches:      475
Percent Similarity: 84.63%      Conservative: 59
Best Local Similarity: 75.28%      Mismatches: 81
Query Match:     75.45%      Indels:      16
DB:              6      Gaps:      6

US-10-025-145A-65 (1-618) x AR2666971 (1-2018)

Qy      1  MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
      Db      6  ATGGCTCTAGTTCTACCGCACCGTTGGCTTCCAATCATGCCTGCACAAATCGTTGATC 65

Qy      16  SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
      Db      66  AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCTAGGAATGAGTAGG 125

Qy      36  ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
      Db      126  CGAGGGAATCTATCACTCCTTCCATCAGCATGAGCTCTACCAACCGTTGTAAACCGATGAT 185

Qy      56  SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
      Db      186  GGTGTACGAAGACGATGGCGATTTCATTCCAACCTCTGGACGATGATGTCAATACAG 245

Qy      76  SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
      Db      246  TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGTGAGAAACTGATC 302

Qy      96  GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
      Db      303  GGGGAAGTAAAGAAC--ATGTTCATTCGATGTCTATTAGAAAGATGGAGAGTTAATGAGT 359

Qy      113  -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
      Db      360  CCGCTCAATGATCTCATTCACCGCCTTTGGATTGTGACAGACGCCCTTGAACGTTTGGGGATC 419

Qy      131  AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
      Db      420  CATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATGTTACAGTTATTGGGGC 479

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Db      1557 ATCCTTCGATTACGAGGTGATACGGGTGCTACAGGCGGACAGGGCTCGTGGAGAAGAA 1616
QY      528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db      1617 GCTTCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676
QY      548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
Db      1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAGAGGATTAATTTGGAACTTCTCAAA 1736
QY      568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db      1737 CCAGACATCAATGTTCCTCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796
QY      588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db      1797 CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG 1856
QY      608 ValMetArgThrValIleGluProValProLeu 618
Db      1857 GTCACGAGAACCCCTCCTTGAATCTGTGCCCTTTG 1889

RESULT 8
AR316320
LOCUS   AR316320                2018 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION   Sequence 19 from patent US 6559297.
ACCESSION   AR316320
VERSION     AR316320.1  GI:31711055
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.

REFERENCE   1 (bases 1 to 2018)
AUTHORS    Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE      Syntheses
JOURNAL    Patent: US 6559297-A 19 06-MAY-2003;
FEATRRS    Location/Qualifiers
SOURCE     1. .2018
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:      2.34e-190      Length:      2018
Score:          2453.00      Matches:      475
Percent Similarity: 84.63%      Conservative: 59
Best Local Similarity: 75.28%      Mismatches: 81
Query Match:      75.45%      Indels:      16
DB:              6      Gaps:      6

US-10-025-145A-65 (1-618) x AR316320 (1-2018)

QY      1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db      6 ATGGCTCTAGTTCTACCGCACCGTTGGCTTCCAAATCATGCTGCACAAATCGTTGATC 65

QY      16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db      66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAATTCACGCTCTAGGAATGAGTAGG 125

QY      36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db      126 CGAGGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACTGTGAACCGATGAT 185

QY      56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db      186 GGTGTACGAAGACGCATGGCGGATTTCCATTCCAACCTCTGGGACGATGATGTCATACAG 245

QY      76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db      246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGGTGCTGAGAAACTGATC 302
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QY      96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db      303 GGGGAAGTAAAGAAC--ATGTTCAATTCGATGTCATTAGAAGATGGAGAGTTAATGAGT 359
QY      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db      360 CCGCTCAATGATCTCATTCACGCCTTTGGATGTGTCGACAGCCTTGAACGTTGGGATC 419
QY      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db      420 CATAGACATTTCAAAGATGAGATAAAATCGGGCGTTGATTATGTTTACAGTTATTGGGC 479
QY      151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db      480 GAAAATGGCATCGGATCGGGAGGGAGAGTGTGTACTGATCTGAACCTCAACTCGCGTTG 539
QY      171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db      540 GGGCTTCGAACCTACGACTACACGGATACCCGGTGTTCTTCAGATGTTTTCAAAGCTTTC 599
QY      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210
Db      600 AAAGGCCAAATCGGCAGTTTTCTCTACCAATATTTAAAGAAGCCCTGCAAAAGATTCGGTCTCC 659
QY      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db      660 GCGGTTCTGAATTTATTCGGGGCTCCCTCATTCGCTTTCCAGGGGAGAAAATTATGGAT 719
QY      231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db      720 GAGGCTGAAATCTTCTACCAATATTTAAAGAAGCCCTGCAAAAGATTCGGTCTCC 779
QY      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db      780 AGT---CTTTCCGAGAGATCGGGACGTTTGGAAATATGTTGGCACACATATTTGCCG 836
QY      271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db      837 CGATTGGAAGCAAGGAATTACATCCAAGTCTTGGACAGGACACTGAGAACACGGAAGTCA 896
QY      291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db      897 TATGTGAAGAGACAAAAAACTTTTAGAACTCGCAAAATTTGGAGTTCAACATCTTTCAATCC 956
QY      308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db      957 TTACAAAAGAGGGAGTTAGAAAGTCTGGTCAGATGGTGGAAAGATCGGGTTTTCTGAG 1016
QY      328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db      1017 ATGACCTTCTGCCGACATCGTCCACGTTGGAATACTACACTTTGGCTTCTCGCATTCGTTTC 1076
QY      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db      1077 GAGCCTCAACATTTCTGGATTCAGACTCGGCTTTGCCAAGACCGTGTCTATTATCACGGTT 1136
QY      368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db      1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACCTCTCACAGCGACA 1196
QY      388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db      1197 ATGAAGAGATGGGATCCGTCTCGATAGATTGCCTTCCAGAATATATGAAAGGAGTGTAC 1256
QY      408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db      1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCGAGAGGGCTCAAGGCCGA 1316
QY      428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db      1317 GATACGCTCACATATGCTCGGGAGCTTGGAGGCTTATATTGATTGTTATATGCAAGAA 1376
QY      448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
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Db      1377 GCAAAGGTGGATCGCCACTGGTTACCTGGCCCTCCTTTGATGAGTACTACGAGAAATGGGAAA 1436
Qy      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db      1437 GTTAGCTGTGGTCATCGCATATCCGCATTGCAACCCATTCTGCAATGGACATCCCCCTTT 1496
Qy      488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db      1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCTTAACGACTTGGCATGTGCC 1556
Qy      508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db      1557 ATCCTTCGATTACGAGGTGATACGGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAA 1616
Qy      528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db      1617 GCTTCCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676
Qy      548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db      1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAAATTGGGAACCTTCTCAA 1736
Qy      568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db      1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACATGCCAGAGCTTTC 1796
Qy      588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db      1797 CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG 1856
Qy      608 ValMetArgThrValIleGluProValProLeu 618
Db      1857 GTCACGAGAACCCCTCCTTGAATCTGTGCGCTTTG 1889

RESULT 9
AR338463
LOCUS      AR338463
DEFINITION Sequence 19 from patent US 6569656.
ACCESSION  AR338463
VERSION    AR338463.1 GI:33725240
KEYWORDS
SOURCE
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 2018)
AUTHORS   Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE     Syntheses
JOURNAL   Patent: US 6569656-A 19 27-MAY-2003;
FEATURES   location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:      2.34e-190      Length:      2018
Score:          2453.00      Matches:      475
Percent Similarity: 84.63%      Conservative: 59
Best Local Similarity: 75.28%      Mismatches: 81
Query Match:    75.45%      Indels:      16
DB:             6      Gaps:      6

US-10-025-145A-65 (1-618) x AR338463 (1-2018)

Qy      1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db      6 ATGGCTTAGTTTCTACCGCACCGTTGGCTTCCAAATCATGCCTGCACAAAATCGTTGATC 65
Qy      16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db      66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATTCACGCTCTAGGAATGAGTAGG 125
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Qy      36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db      126 CGAGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACCGTTGTAACCGATGAT 185
Qy      56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db      186 GGTGTACGAAGACGCATGGCGATTTCATTCCACCTCTCGGACGATGATGTATACAG 245
Qy      76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db      246 TCITTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTCTGAGAACTGATC 302
Qy      96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db      303 GGGGAAGTAAAGAAC--ATGTTCAATTTCGATGTCTATTAGAGATGGAGAGTTAATGAGT 359
Qy      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeuGlyIle 130
Db      360 CCGCTCAATGATCTCATTCAACGCCTTTGGATTGTCACAGCCTTGAACGTTTGGGGATC 419
Qy      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db      420 CATAGACATTTCAAAGATGAGATAAAATCGCGCTTGATTATGTTTACAGTTATTGGGC 479
Qy      151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db      480 GAAAAATGGCATCGGATCGGGAGGAGAGTGTGTTACTGATCTGAACCTCAACTGCGTTG 539
Qy      171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db      540 GGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTCAAAGCTTTC 599
Qy      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210
Db      600 AAAGGCCAAAATGGGCAGTTTTCTCTGCTCTGAAAATATTTACAGACAGATGAAGAGATCAGA 659
Qy      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db      660 GGCCTTCTGAATTTATTCCGGGCTCCCTCATTGCCTTTCCAGGGAGAAAAATTATGGAT 719
Qy      231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db      720 GAGGCTGAAAATCTTCTCTACCAAATATTTAAAGNAGCCCTGCAAAAGATTCGGGTCTCC 779
Qy      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270
Db      780 AGT---CTTTCGGAGAGATCGGGACGTTTGGAAATATGGTTGGCACACATATTTCGCCG 836
Qy      271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db      837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTTGGACAGGACACTGAGAACACGGAAGTCA 896
Qy      291 -----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307
Db      897 TATGTGAAGAGCAAAAACCTTTTAGAACTCGCAAAATTGGAGTTCAACATCTTTCAATCC 956
Qy      308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db      957 TTACAAAAGAGGGAGTTAGAAAGTCTGGTCAGATGGTGGAAAGAAATCGGGTTTTCCTGAG 1016
Qy      328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db      1017 ATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTGGCTTTCCTGCAATTCGCTTC 1076
Qy      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db      1077 GAGCCTCAACATTTCTGGATTACAGACTCGGCTTTGCCAAGACGCTGTCATCTTATCACGGTT 1136
Qy      368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db      1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACA 1196
Qy      388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
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Db	1197	ATGAAGAGATGGGATCCGTCCTCGATAGATTGCCTTCCAGAAATATATGAAAGGAGTGTAC	1256
Qy	408	MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg	427
Db	1257	ATAGCGGTTTACGACACCGCTAAATGAAATGGCTCGAGAGGCGAGAGGCTCAAGGCCGA	1316
Qy	428	AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu	447
Db	1317	GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTCGTATATGCAAGAA	1376
Qy	448	AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys	467
Db	1377	GCAAGGTGGATCGCCACTGGTTACCTGCGCATTCCTTTGATGAGTACTACGAGATGGGAAA	1436
Qy	468	ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe	487
Db	1437	GTTAGCTGTGGTCATCGCATATCCGCATTGCAACCCATTCTGACAAATGGACATCCCCCTT	1496
Qy	488	ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle	507
Db	1497	CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCTTAACGACTTGGCATGTGCC	1556
Qy	508	IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu	527
Db	1557	ATCCTTCGATTACGAGGTGATACGCGGTGCTACAAGGCGGACAGGGCTCGTGGAGAAGAA	1616
Qy	528	AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu	547
Db	1617	GCTTCCTCTATATCATGTTATATGAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTC	1676
Qy	548	AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys	567
Db	1677	GATCATATCAACGCCATGATCAGTGACGCTAATCAAAGGATTAAATTGGGAACCTTCTCAA	1736
Qy	568	ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp	587
Db	1737	CCAGACATCAATGTTTCCCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC	1796
Qy	588	HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu	607
Db	1797	CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGGAAGATTG	1856
Qy	608	ValMetArgThrValIleGluProValProLeu	618
Db	1857	GTCACGAGAACCCCTCCTTGAATCTGTGCTTTG	1889
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
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ORIGIN			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			

DB:	6	Gaps:	6
US-10-025-145A-65 (1-618) x AR429869 (1-2018)			
Qy	1	MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu-----	15
Db	6	ATGGCTCTAGTTTCTACCGCACCGTTGGCTTCCAAATCATGCCTGCACAAATCGTTGATC	65
Qy	16	SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg	35
Db	66	AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCTAGGAATGAGTAGG	125
Qy	36	ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp	55
Db	126	CGAGGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACTGTGTAAACCGATGAT	185
Qy	56	SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln	75
Db	186	GGTGTAAGAAGACGATGGGCGATTTCATTCCAACTCTGGGACGATGATGTATACAG	245
Qy	76	SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle	95
Db	246	TCITTTA--CCAACGGCTTATAGGAAAAAATCGTACCTGGAGCGTGTGAGAAACTGATC	302
Qy	96	GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly-----	112
Db	303	GGGGAAGTAAAGAAC--ATGTTCAATTGATGTCATTAGAGAATGGAGAGTTAATGAGT	359
Qy	113	-----AsnAspLeuLeuGlnArgLeuLeuLeuValAspValGluArgLeuGlyIle	130
Db	360	CCGCTCAATGATCTCATTCACGCGCTTTGGATTGTCGACAGCCCTGAACGTTGGGGATC	419
Qy	131	AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn	150
Db	420	CATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATGTTTACAGTTATTGGGGC	479
Qy	151	GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu	170
Db	480	GAAATGGCATCGGATCGGGAGGAGAGTGTGTTACTGATCTGAACTCAACTGCGTTG	539
Qy	171	GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe	190
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Qy	191	LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg	210
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Db	660	GGCGTTCTGAATTTATTCGGGGCTTCCCTCATTTGCCCTTCCAGGGGAGAAATATGGAT	719
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Db	720	GAGGCTGAAATCTTCTCTACCAAATATTTAAAGAACCCCTGCAAAAGATTCCGGTCTCC	779
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Qy	271	ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla	290
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Qy	291	-----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer	307
Db	897	TATGTGAAGAGCAAAAACCTTTTAGAACTCGCAAAATTTGGAGTTCAACATCTTTCAATCC	956
Qy	308	LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu	327
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Qy	328	MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe	347



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Db 1197 ATGAAGAGATGGGATCCGTCCTCGATAGATTGCCTTCCAGAAATATATGAAAGGAGTGTAC 1256

QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427

Db 1257 ATAGCGGTTTACGACACCGTAAATGGCTCGAGAGGCGAGAGGCTCAAGGCCGA 1316

QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447

Db 1317 GATACGCTCACATATGCTCGGAAGCTTCGGAGGCTTATATTGATTCTATATGCAAGAA 1376

QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1377 GCAAGGTGGATCGCCACTGGTTACCTGCCTCCTTTGATGAGTACTACGAGAATGGGAAA 1436

QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487

Db 1437 GTTAGCTGTGTCATCGCATATCCGCAATTGCAACCCATTCTGACAAATGGACATCCCTTT 1496

QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507

Db 1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCTTAACGACTTGGCATGTGCC 1556

QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527

Db 1557 ATCCTTCGATTACGAGGTGATACGCGGTGCTACAAGGCGGACAGGCTCGTGGAGAAGAA 1616

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Db 1617 GCTTCCTCTATATCATGTTATATGAAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676

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Db 1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAAATTGGGAACCTTCTCAA 1736

QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587

Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACATGCCAGAGCTTTC 1796

QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607

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RESULT 11

AGU87909

LOCUS AGU87909 2018 bp mRNA linear PLN 24-SEP-1997

DEFINITION Abies grandis pinene synthase (AG3.18) mRNA, complete cds.

ACCESSION U87909

VERSION U87909.1 GI:2411482

KEYWORDS

SOURCE

ORGANISM

Abies grandis

Abies grandis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.

1 (bases 1 to 2018)

REFERENCE

AUTHORS Bohlmann,J., Steele,C.L. and Croteau,R.

TITLE Monoterpene synthases from grand fir (Abies grandis). cDNA

isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase

J. Biol. Chem. 272 (35), 21784-21792 (1997)

97413772

9268308

2 (bases 1 to 2018)

Bohlmann,J., Steele,C.L. and Croteau,R.

Direct Submission

Submitted (31-JAN-1997) Institute of Biological Chemistry, Washington State University, Clark Hall, Pullman, WA 99164-6340, USA

FEATURES

source

gene

CDS

Location/Qualifiers

1..2018

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1..2018

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6..1892

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ORIGIN

Alignment Scores:

Pred. No.: 2,34e-190 Length: 2018

Score: 2453.00 Matches: 475

Percent Similarity: 84.63% Conservative: 59

Best Local Similarity: 75.28% Mismatches: 81

Query Match: 75.45% Indels: 16

DB: 8 Gaps: 6

US-10-025-145A-65 (1-618) x AGU87909 (1-2018)

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Db 6 ATGGCTCTAGTTTCTACCGCACCGTTGGCTTCCAAATCATGCCTGCACAAATCGTTGATC 65

QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35

Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCTAGGAATGAGTAGG 125

QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55

Db 126 CGAGGAAATCTATCACTCTCTCCATCAGCATGAGCTCTACACCGTGTAAACCGATGAT 185

QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75

Db 186 GGTGTACGAAGACGCATGGCGGATTTCCTCCAACTCTGGACGATGATGTCATACAG 245

QY 76 SerLeulleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95

Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAAATCGTACCTGGAGCGTCTGAGAACTGATC 302

QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112



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ORIGIN

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Query Match: 71.62% Indels: 19  
DB: 8 Gaps: 8

US-10-025-145A-65 (1-618) x AF543527 (1-2082)

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QY	35	ArgProGlyLysSerValAlaHis---SerIleAsnMetCysLeuThrSerValAlaSer	53
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QY	54	ThrAspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPhe	73
Db	212	GATGATGCTGTATTAAAGACGCAGAGGTGATTTCCATTCCAACCTCTGGGACGATGTTG	271
QY	74	IleGlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArg	93
Db	272	ATACAGTCCCTT---TCCTCGCCTTATGGGAAACCCTCTTATCGGAAACGTGTGAGAGA	328
QY	94	LeuIleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly---	112
Db	329	CTGATTGGGGAAGTAAAGAAT--AGCTTCAATTCAATGTCAAAACGAAGATGCGGAATCA	385
QY	113	-----AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeu	128
Db	386	ATCACTCCCTCGATGATCTGATTCAACGCCCTTTGGATGGTCGACAGTGTTGAACGTTTG	445
QY	129	GlyIleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyr	148
Db	446	GGAATCGACAGACATTTCAAAAAAGAGATAAAATCAGCGCTCGATCATGTTTACAGGTAT	505
QY	149	TrpAsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThr	168
Db	506	TGGAGCGAAAAAGGCATTGGATGTGGGAGAGAGAGTGTGTACTGACCTCAACTCAACT	565
QY	169	AlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsn	188
Db	566	GCCTTGGGTCTTCGAACCTTCGTCTGCACGGATACGATGTGTCTGCAGACGCTTTTGAAT	625
QY	189	ValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGlu	208
Db	626	CATTTCAAAAATCAAAGTGGCAGTTTGCTTGCACTCTGAAG---CAGACAGAGGATCAG	682
QY	209	IleArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysVal	228
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QY	229	MetAspGluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIlePro	248
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QY	249	AlaSerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsn	268
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QY	269	LeuProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLys	288
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QY	289	AsnAla-----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePhe	305
Db	920	AAGTCATATATGAAGACCGAGAAACTTCTCGAACTTGCAAAGTTGGAGTTCAACATCTTT	979
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VERSION      AF543529.1  GI:28894485
KEYWORDS
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REFERENCE      1 (bases 1 to 2162)
AUTHORS      Phillips,M.A., Wildung,M.R., Williams,D.C., Hyatt,D.C. and
              Croteau,R.
TITLE      cDNA isolation, functional expression, and characterization of
              (+)-alpha-pinene synthase and (-)-alpha-pinene synthase from
              loblolly pine (Pinus taeda): Stereocontrol in pinene biosynthesis
JOURNAL      Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
MEDLINE      22510022
PUBMED      12623076
REFERENCE      2 (bases 1 to 2162)
AUTHORS      Phillips,M.A., Wildung,M.R., Williams,D.C. and Croteau,R.B.
TITLE      Direct Submission
JOURNAL      Submitted (09-SEP-2002) Institute of Biological Chemistry,
              Washington State University, PO Box 646340, Pullman, WA 99164-6340,
              USA
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US-10-025-145A-65 (1-618) x AF543529 (1-2162)
QY      1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db      59 ATGGATTTAATATCTGTCTTACCGTCGGCTTCCAAATCGTGTGTGCGCTGCACAAACCC 118
QY      16 -----SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIle 33
Db      119 TTGAGTAGTTCTACTATAAACTTAAGCCTTTCTGCAAAACAATCCGATTCTTGTAAATG 178
QY      34 CysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSer 53
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Db      179 CCGAGGCGATGGGAATTGCCAGGCCGTCC-----ATGAGTCTGAGTACCGTTGCATCT 232
QY      54 ThrAspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPhe 73
Db      233 GAAGATGATATACAAAGACGCACGGCGGTTATCTTCCAACCTGTGGAACGATGATGTG 292
QY      74 IleGlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArg 93
Db      293 ATACAG--TTTCTGTCAACGCCTTATGGGAACTCGCTTACCGTGAACGTGCTGAGCGA 349
QY      94 LeuIleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly--- 112
Db      350 CTGATTGATGAAGTAAGGGACATA--TTCACTTCGATGTCATTGGAAGATGGAGAATTC 406
QY      113 AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeuGlyIleAspArg 132
Db      407 AGTGATCTCATTCACGCCCTTTGGATGGTTCGATAACGTTGAACGTTTGGGGATCGATAGG 466
QY      133 HisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsnGluLys 152
Db      467 CATTTCAAAATGAGATCAAATCAGCGCTTGATATGTTTACAGTTACTGGAGCGCAAAA 526
QY      153 GlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeuGlyLeu 172
Db      527 GGCATTGGATGTGGACAAAAAGTATTATTACTAATCTCAATTCAACTGCCTGGGCTTT 586
QY      173 ArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPheLysAsp 192
Db      587 CGAACTCTTCGATTACACGGATACCCCTGTTCTGCAGACGTTTGAACATTTCAGAAAC 646
QY      193 LysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArgGlyVal 212
Db      647 CAAATTGGGCAGTTGTATCATGTCCCTAGT---GAGACAGAGGAAGACATAAGAATCATG 703
QY      213 LeuAsnLeuPheArgAlaSerLeu-----ValAlaPheProGlyGluLysVal 228
Db      704 GTCAATTTATATCGGGCTTCCCTCATTTGCCGTTTCCCGGTGAGAAAGTT 763
QY      229 MetAspGluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIlePro 248
Db      764 ATGGAAGAGGCAGAAAGCTTCTCAGAGAAATATTTAAAGGAAACTCTGCAAAAGATTCCG 823
QY      249 AlaSerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsn 268
Db      824 GACTGCAGT---CTTCAAGAGAGATAGGGACGTTTGAACATGTTGGCACACAAAT 880
QY      269 LeuProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsn--- 287
Db      881 TTGCCGCGATTAGAAGCAAGGAATTACATCGACGTCTTCGGACAAGACACTAAGAAATATG 940
QY      288 -----LysAsnAlaAlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePhe 305
Db      941 GAGCCAAATAGGAAGACGGAGAAACTGTAGAACTTGCAAACTGGAGTTCAACATCTTT 1000
QY      306 HisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySer 325
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QY      326 ProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIle 345
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QY      346 AlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIle 365
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QY      366 ThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThr 385
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QY	426	GlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMet	445
Db	1361	GGCCGAGACACTCTCAACTATGTCTCGACAGGCTGGGAGGATTGTCTGATTACATATG	1420
QY	446	GlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsn	465
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QY	466	GlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIle	485
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QY	486	ProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIle	505
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QY	506	CysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGly	525
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QY	526	GluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAsp	545
Db	1661	GAAGAAACCTCCTGTATATCTTGTATATGAAAGACAATCCTGGAGCAACAGAGGAAGAT	1720
QY	546	AlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeu	565
Db	1721	GCTCTTAATCATCTCAACGTCATGATCAGTGGCGTAATTAAAGAAATTAATTTGACATTACCAGA	1780
QY	566	LeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArg	585
Db	1781	CTCAAAACCCAAACAGCAGTGTGCCCATTTCTTCCAAGAAAAATTAATTTGACATTACCAGA	1840
QY	586	ValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLys	605
Db	1841	GCTTTCCATTACGGTTACAAATACCGAGATGGCTACAGCGTTTCCAGCGTTTGAACAAAG	1900
QY	606	SerLeuValMetArgThrValIleGluProValProLeu	618
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Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			

US-10-025-145A-65 (1-618) x AR222137 (1-2186)			
QY	1	MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu-----	15
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QY	16	---SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCys	34
Db	85	AGTCTACTCATCATGAGCTCAAGCCTCTGCGCAGAACCATCCCAACTCTTGGAAATGTGT	144
QY	35	ArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr	54
Db	145	AGCGAGGAAAAATCTTTCACACCTTCTCTGAGCATGAGTTTGACCACCGCTGTATCTGAT	204
QY	55	AspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIle	74
Db	205	GATGGTCTACAAAGACGCATAGGTGACTATCATTTCCAATCTCTGGGACGACGATTTTATA	264
QY	75	GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu	94
Db	265	CAGTCTCTA---TCAACGCCCTTATGGGAGCCCTTCTTACCGAGAACGTGCTGAGAAACTG	321
QY	95	IleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly-----	112
Db	322	ATTGGGGAAGTGAAGGAG--ATGTTCAATTCAATGCCATCGGAAGATGGAGAAATCAATG	378
QY	113	-----AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeuGly	129
Db	379	AGTCCCTCAATGATCTTATTGAACGACTTTGGATGGTCGATAGCTTGAACGTTTGGGG	438
QY	130	IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrp	149
Db	439	ATTGATAGACATTTCAAAAAAGAGATAAAATCAGCCCTTGATTATGTTTACAGTTATTGG	498
QY	150	AsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla	169
Db	499	AACGAAAAAGGTATTGGATCGGTAGAGATAGTGTTTTTCCTGATGTCAACTCGACTGCC	558
QY	170	LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnVal	189
Db	559	TCGGGGTTTCGAACCTCTTCGCCTACACGGATACAGTGTCTCTTCAGAGGTTTGAAGTA	618
QY	190	PheLysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIle	209
Db	619	TTTCAAGACCAAAATGGGCAGTTTGCATTCTCTCCTAGTACAAA--GAGAGAGACATC	675
QY	210	ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMet	229
Db	676	AGAACCGTTCTGAATTATATCGGGCTTCTTTCATTGCCTTTCCTGGGAGAAAAGTTATG	735
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QY	270	ProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThr-----	285
Db	853	CCAAGATTGGAAACAAGGAATTACTTAGATGTATTTGGACATCTCACCAGTCCATGGCTC	912
QY	286	LysAsnLysAsnAla-----AlaGluLysLeuLeuGluLeuAlaLysLeuGlu	301
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QY	322	AspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeu	341



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QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeuGly 129  
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QY 130 IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrp 149  
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QY 190 PheLysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIle 209  
Db 619 TTTCAGAGCCAAAATGGGCAGTTTGTCATTTCTCTCCTAGTACAAAA---GAGAGAGACATC 675  
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QY 270 ProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThr----- 285  
Db 853 CCAAGATTGGAACAAGGAATTACTTAGATGTATTGGACATCTCTACCAGTCCATGGCTC 912  
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QY 342 AlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMet 361  
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QY 402 TyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAla 421  
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QY 522 ArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeu 541  
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Search completed: July 8, 2004, 19:20:23  
Job time : 6830 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 8, 2004, 12:19:34 ; Search time 707 Seconds  
(without alignments)  
3713.418 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRCLSSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
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6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3251	100.0	2013	4	AAF73411	Aaf73411 Grand fir
2	2453	75.5	2018	2	AAx08644	Aax08644 Pinene sy
3	2453	75.5	2018	3	AAa38922	Aaa38922 Grand fir
4	2453	75.5	2018	4	AAf73372	Aaf73372 Grand fir
5	2264	69.6	2186	4	AAf73412	Aaf73412 Grand fir
6	2200.5	67.7	2196	2	AAx08643	Aax08643 Myrcene s
7	2200.5	67.7	2196	3	AAa38927	Aaa38927 Grand fir
8	2200.5	67.7	2196	4	AAf73371	Aaf73371 Grand fir

9	2197.5	67.6	2205	2	AAx08663	Aax08663 Grand fir
10	2197.5	67.6	2205	4	AAf73391	Aaf73391 Grand fir
11	2137	65.7	1890	4	AAf73421	Aaf73421 Grand fir
12	2084.5	64.1	2429	4	AAf73413	Aaf73413 Grand fir
13	2031.5	62.5	2089	2	AAx08645	Aax08645 Limonene
14	2031.5	62.5	2089	3	AAA38938	Aaa38938 Grand fir
15	2031.5	62.5	2089	4	AAf73373	Aaf73373 Grand fir
16	1617.5	49.8	1513	3	AAA69551	Aaa69551 Pinus rad
17	1611.5	49.6	1634	3	AAA69644	Aaa69644 Pinus rad
18	1295.5	39.8	1865	2	AAa38933	Aaa38933 Grand fir
19	1295.5	39.8	1885	2	AAx87534	Aax87534 Delta-sel
20	1295.5	39.8	1885	2	AAx87533	Aax87533 Delta-sel
21	1295.5	39.8	1888	2	AAx87505	Aax87505 Grand fir
22	1291.5	39.7	1885	2	AAx87532	Aax87532 Delta-sel
23	1267.5	39.0	1173	3	AAA69643	Aaa69643 Pinus rad
24	1250.5	38.5	1967	2	AAx87513	Aax87513 Grand fir
25	1250.5	38.5	1967	2	AAx08655	Aax08655 Grand Fir
26	1250.5	38.5	1967	4	AAf73383	Aaf73383 Grand fir
27	1240.5	38.2	2700	2	AAT97447	Aat97447 Pacific y
28	1240.5	38.2	2700	3	AAA38931	Aaa38931 Yew taxed
29	1231	37.9	1785	2	AAx87535	Aax87535 Gamma-hum
30	1231	37.9	1785	3	AAA38934	Aaa38934 Grand fir
31	1231	37.9	1977	2	AAx87506	Aax87506 Grand fir
32	1230	37.8	1785	2	AAx87536	Aax87536 Gamma-hum
33	1230	37.8	1785	2	AAx87537	Aax87537 Gamma-hum
34	1188.5	36.6	2528	2	AAx87529	Aax87529 Grand fir
35	1187	36.5	2424	2	AAx08654	Aax08654 Grand Fir
36	1187	36.5	2424	3	AAA38932	Aaa38932 Grand fir
37	1187	36.5	2424	4	AAf73382	Aaf73382 Grand fir
38	1187	36.5	2525	2	AAx87530	Aax87530 E-alpha-b
39	1187	36.5	2528	2	AAx87531	Aax87531 E-alpha-b
40	1187	36.5	2571	2	AAx87504	Aax87504 Grand fir
41	1052.5	32.4	2861	3	AAA38937	Aaa38937 Grand fir
42	856	26.3	696	4	AAf73414	Aaf73414 Grand fir
43	829.5	25.5	779	3	AAA69642	Aaa69642 Pinus rad
44	800	24.6	1416	2	AAx08656	Aax08656 Grand Fir
45	800	24.6	1416	4	AAf73384	Aaf73384 Grand fir

ALIGNMENTS

RESULT 1  
AAF73411  
ID AAF73411 standard; cDNA; 2013 BP.  
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AC AAF73411;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 64.  
DE Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
(UNIW ) UNIV WASHINGTON STATE RES FOUND.  
PA Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
XX WPT; 2001-182782/18.  
DR P-PSDB; AAB69390.  
XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene

PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.

PS Claim 8; Page 147-149; 175pp; English.

XX The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants

SQ Sequence 2013 BP; 591 A; 432 C; 464 G; 526 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 2013  
Score: 3251.00 Matches: 618  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-025-145A-65 (1-618) x AAF73411 (1-2013)

QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeuSerSerSerHisGlu 20  
|||  
Db 36 ATGGCTCTTCTTCTATTACTCGCTGGTTCCAGGTCGTGCTCAGTTCTTCTCATGAG 95  
  
QY 21 IleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArgProGlyLysSerVal 40  
|||  
Db 96 ATTAAGGCTCTCCGTAGAACAAATCCCAACTCTTTGGAATCTGCAGGCCGGGAAATCCGTC 155  
  
QY 41 AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg 60  
|||  
Db 156 GCGCATTCCTAAACATGTGTTTGACAAGCGTCGTCATCTACTGATTTCTGTACAGAGACGC 215  
  
QY 61 ValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGlnSerLeuIleSerThr 80  
|||  
Db 216 GTGGGCAACTATCATTCCAACCTGTGGGACGATGATTTTCATACAGTCTCTGATCTCAACG 275  
  
QY 81 ProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyGluValLysAsp 100  
|||  
Db 276 CCTTATGGAGCACCTGATTACCGGGAACGTGCTGACAGACTTATTGGGGAAGTAAAGGAT 335  
  
QY 101 IleMetPheAsnPheLysSerLeuGluAspGlyGlyAsnAspLeuLeuGlnArgLeuLeu 120  
|||  
Db 336 ATAATGTTCAATTCAAGTCGCTGGAAGATGGAGGCAATGATCTCCTTCAACGACTTTTG 395  
  
QY 121 LeuValAspAspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThr 140  
|||  
Db 396 CTGGTCGATGACCTGTAACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACG 455  
  
QY 141 AlaLeuAspTyrValAsnSerTyrTrpAsnGluLysGlyIleGlyCysGlyArgGluSer 160  
|||  
Db 456 GCACCTCGATTATGTTAAACAGTTATTGGAAACGAAAAAGGCATTTGGATGTGGGAGGAGAT 515  
  
QY 161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr 180  
|||  
Db 516 GTTGTGACTGACTGACTCAACTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATAC 575  
  
QY 181 ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr 200  
|||  
Db 576 ACTGTGCTCTCAGATGTTTGAACGTTTAAAGACAAAAATGGGCAATTTTCTCCACT 635  
  
QY 201 AlaAsnIleGlnIleGluGlyGluIleArgGlyValLeuAsnLeuPheArgAlaSerLeu 220  
|||  
Db 636 GCCAATATTACAGATAGAGGGAGAGATTAGAGCGGTTCTCAATTTATTACGGCCCTCCCTC 695  
  
QY 221 ValAlaPheProGlyGluLysValMetAspGluAlaGluThrPheSerThrLysTyrLeu 240  
|||  
Db 696 GTCGCCTTTCCCGCGAGAAAGTTATGGATGAGCTGAAACATTTCTCTACAAAATATTTA 755

QY 241 ArgGluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal 260  
|||  
Db 756 AGAGAAAGCCCTGC AAAAGATTCCGGCATCCAGTATACTTTCTACATAGATACGGACGTT 815  
  
QY 261 LeuGluTyrGlyTrpHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal 280  
|||  
Db 816 CTGGAATATGGTTGGCACACCAATTGGCACCGCTTGGAAAGCAAGGAATTACATGACGTC 875  
  
QY 281 PheGlyGlnHisThrLysAsnLysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeu 300  
|||  
Db 876 TTTGGACAGCACACTAAAAATAAGAACGCCGCCGAGAAAACCTTTTAGAACTTGCAAAATTG 935  
  
QY 301 GluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrp 320  
|||  
Db 936 GAATTCAATATATTTCACCTCCTTACAGAGAGAGAGTTAAAACATGTTTCCCGATGGTG 995  
  
QY 321 LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla 340  
|||  
Db 996 AAAGACTCGGGTTCTCTGAGATGACCTTCTGTGCACATCGTCACGTGGAATACTACGCT 1055  
  
QY 341 LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLys 360  
|||  
Db 1056 TTGGCTTCCTGCAATTGCGTTCGAGCCCTCAACATTTCTGGATTCAGACTTCGGCTTTACCAAG 1115  
  
QY 361 MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu 380  
|||  
Db 1116 ATGTCTCATCTTATCACGGTTCCTGACGACATGTACGACGTCTTCGGCACAGTAGACGAG 1175  
  
QY 381 LeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuPro 400  
|||  
Db 1176 CTGGAACCTTTCACAGCGACAAATTAAGAGATGGGATCCGTCGCGATGGAATGCCTTCCA 1235  
  
QY 401 GluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal 420  
|||  
Db 1236 GAATATATGAAAGGAGTGTACATGATGGTTTATCACACCGTAAATGAATGGCTCGAGTG 1295  
  
QY 421 AlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCys 440  
|||  
Db 1296 GCAGAGAAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGT 1355  
  
QY 441 PheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlu 460  
|||  
Db 1356 TTTGATTCGTATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAG 1415  
  
QY 461 GluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle 480  
|||  
Db 1416 GAGTACTTGGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATT 1475  
  
QY 481 LeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLys 500  
|||  
Db 1476 CTGACGTTGGACATCCCTTTCCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAG 1535  
  
QY 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAla 520  
|||  
Db 1536 CTCAATGACTTGATATGATCATCTTCGATTAAAGAGGTGATACACGGTGCTACAAGGCA 1595  
  
QY 521 AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGly 540  
|||  
Db 1596 GACAGGGCCCGTGGAGAAAGACTTCGTCATATATCATGTTATATGAAAGACAATCCTGGA 1655  
  
QY 541 LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu 560  
|||  
Db 1656 TTAACGGAAGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGGCGCAATCAGAGAA 1715  
  
QY 561 LeuAsnTrpGluLeuLysProAspAsnSerValProIleThrSerLysLysHisAla 580  
|||  
Db 1716 TTAAATTGGGAGCTTCTAAAGCCAGACACAGTGTTCCTCATCTCCAAGAAACACGCA 1775  
  
QY 581 PheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAla 600  
|||  
Db 1776 TTTGACATAAGCACAGATTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCC 1835

QY 601 AsnValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618  
|||||  
Db 1836 AACGTTGAAACAAAGAGTTTGGTGATGAGAACCGTCATTGAACCTGTGCCTTTG 1889  
RESULT 2  
AAX08644  
ID AAX08644 standard; cDNA; 2018 BP.  
XX  
AC AAX08644;  
XX  
DT 27-SEP-1999 (first entry)  
XX  
DE Pinene synthase gene.  
XX  
KW Mycrene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.  
XX  
OS Abies grandis.  
XX  
FH Location/Qualifiers  
FT 6..1892  
FT /\*tag= a  
FT /product= "Pinene synthase"  
XX  
PN WO9902030-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014528.  
XX  
PR 11-JUL-1997; 97US-0052249P.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Bohlmann J, Steele CL, Croteau RB;  
XX  
DR WPI; 1999-120396/10.  
DR P-PSDB; AAW85701.  
XX  
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. mycrene, limonene or pinene.  
XX  
PS Claim 10; Page 74-77; 121pp; English.  
XX  
CC Nucleotide sequences encoding mycrene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by mycrene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal  
SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1-2e-243 Length: 2018  
Score: 2453.00 Matches: 475  
Percent Similarity: 84.63% Conservative: 59  
Best Local Similarity: 75.28% Mismatches: 81  
Query Match: 75.45% Indels: 16  
DB: 2 Gaps: 6  
US-10-025-145A-65 (1-618) x AAX08644 (1-2018)  
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
Db 6 ATGGCTCTAGTTCTACCGCACCGTTGGCTTCCAAATCATGCTGCACAAATCGTTGATC 65  
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35

Db |||||:::|||||:::||||| ||||| ||||| |||||::: |||  
66 AGTTCACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGTCTTAGGAATGAGTAGG 125  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
|||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
126 CGAGGGAATCTATCACTCCTTCCATCAGCATGAGCTCTACCAACCGTTGTAACCGATGAT 185  
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIleGln 75  
|||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
Db 186 GGTGTACGAAGACGCATGGCGGATTTCATTCCAACCTCTGGACGATGATGCATACAG 245  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 246 TCCTTA--CCAACGGCTTATGAGGAAAAAATCGTACCTGGAGCGTGTGAGAACTGATC 302  
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTTCGATGTCATTAGAAGATGGAGAGTTAATGAGT 359  
QY 113 -----AsnAspLeuGlnArgLeuLeuValAspValGluArgLeuGlyIle 130  
|||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
Db 360 CCGCTCAATGATCTCATTCACGCCCTTTGGATTGTCACAGCCCTGAACGTTGGGGATC 419  
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 420 CATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATGTTTACAGTTATTGGGGC 479  
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 480 GAAATGCGCATCGGATCGGGAGGAGAGTGTGTTACTGATCTGAACCTCAACTGCGTTG 539  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 540 GGGCTTCGAACCCCTACGACTACACGATACCGGATACCGGTGTCTTCAGATGTTTCAAAGCTTTC 599  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210  
||| |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
Db 600 AAAGGCCAAAATGGGCAGTTTTCTCTGCTCTGAAATATTTCAAAGATGAGAGATCAGA 659  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 660 GCGCTTCTGAATTTATTCGGGGCTCCCTCATTTGCCCTTTCAGGGGAGAAAATTATGGAT 719  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 720 GAGGCTGAAATCTTCTACCAAAATATTTAAAGAACCCCTGCAAAAGATTCCGGTCTCC 779  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 780 AGT---CTTTCGCGAGAGATCGGGACGTTTGGGAATATGTTGGCACACATATTTGCCG 836  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 837 CGATTGGAAGCAAGGAATTACATCCAAGTCTTTGGACAGGACACTGAGAACACGGAAGTCA 896  
QY 291 -----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307  
|||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
Db 897 TATGTGAAGAGCAAAAACCTTTTAGAACTCGCAAAATTTGGAGTTCAACATCTTTCAATCC 956  
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327  
|||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
Db 957 TTACAAAAGAGGGAGTTAGAAAGTCTGGTCAGATGGTGGAAAGAAATCGGGTTTTCTCGAG 1016  
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1017 ATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTGGCTTCCTGCATTTGCGTTC 1076  
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1077 GAGCCTCAACATTTCTGGATTACAGACTCGGCTTTGCCAAGACGTCGTTCATCTTATCACGGTT 1136  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||



Db 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACA 1196

QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407

Db 1197 ATGAAGAGATGGGATCCGTCCTCGATAGATTGCCCTTCAGAAATATATGAAAGGAGTGTAC 1256

QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427

Db 1257 ATAGCGGTTTACGACACCGCTAAATGAATGGCTCGAGAGGCAGAGGCTCAAGGCCGA 1316

QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447

Db 1317 GATACGCTCACATATGCTCGGAAGCTTGGGAGGCTTATATTGATTCGTATATGCAAGAA 1376

QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1377 GCAAGGTGGATCGCCACTGGTTACCTGCCCTCCTTTGATGAGTACTACGAGAATGGGAA 1436

QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487

Db 1437 GTTAGCTGTGGTCATCGCATATCCGCAFTTGAACCCATTCTGACAATGGACATCCCTTT 1496

QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507

Db 1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAACGACTTGGCATGTGCC 1556

QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527

Db 1557 ATCCTTCGATTACGAGGTGATACCGCGTGCTACAAGCGGCAGAGGCTCGTGGAGAGAA 1616

QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547

Db 1617 GCTTCCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676

QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567

Db 1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAATTCGGAACCTTCTCAA 1736

QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587

Db 1737 CCAGACATCAATGTTCCTCATCTCGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796

QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607

Db 1797 CATTACGGGTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG 1856

QY 608 ValMetArgThrValIleGluProValProLeu 618

Db 1857 GTCACGAGAACCCCTCCTTGAATCTGTGCCTTTG 1889

RESULT 3

AAA38922

ID AAA38922 standard; DNA; 2018 BP.

XX AAA38922;

AC AAA38922;

XX 25-AUG-2000 (first entry)

DT 25-AUG-2000 (first entry)

XX Grand fir pinene synthase DNA sequence SEQ ID NO:19.

DE

XX Synthase; protein co-ordinate data; active site; modification; terpenoid;

KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;

KW isoprenoid; breeding programme; fragrance; flavour; pheromone;

KW defensive agent; pigment; antitumour; steroid hormone;

KW signal transduction pathway; bile acid; affinity purification;

KW photoreceptor; enzymatic synthesis; nutrient supplement;

KW immunological reagent; ds.

XX

OS Abies grandis.

XX WO200017327-A2.

PN

XX 30-MAR-2000.

PD

XX 17-SEP-1999; 99WO-US021419.

PF

XX 18-SEP-1998; 98US-0100993P.

XX

PR 22-APR-1999; 99US-0130628P.

PR 23-AUG-1999; 99US-0150262P.

XX (KENT ) UNIV KENTUCKY RES DEPT.

PA (SALK ) SALK INST BIOLOGICAL STUDIES.

XX

PI Chappell J, Manna KR, Noel JP, Starks CM;

XX

DR WPI; 2000-292839/25.

DR P-PSDB; AAY90837.

XX

PT Novel terpene synthase enzymes, useful for producing terpene

PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known

PT enzymes by specific amino acid alterations.

XX

PS Disclosure; Page 363-366; 450pp; English.

XX

CC The present invention describes an isolated terpene synthase (I)

CC comprising a region with at least 20% identity to region 265-535 of a 548

CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha

CC -carbon atoms (alphaC) that have interatomic distances, between each

CC other, within tabulated ranges, have a centre point (within a sphere of

CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered

CC arrangement of R groups (defining aa side chains), excluding specific

CC tabulated arrangements (tables given in the specification). (I), and

CC related enzymes, are used to produce a wide range of terpenoids (e.g.

CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,

CC flavours, pheromones, defensive agents, pigments, antitumour agents,

CC components of signal transduction pathways, precursors of steroid

CC hormones and bile acids, as photoreceptors and as co-factor side chains.

CC Some synthases with little or no catalytic activity (and nucleic acids

CC encoding them) are used as controls in the analysis of products formed by

CC enzymatic synthesis; as nutrient supplements; for affinity purification

CC of isoprenoids; or to develop immunological reagents or nucleic acids for

CC monitoring expression of terpene synthase or inheritance of the gene in

CC plant breeding programs. The new synthases may produce novel terpene

CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent

CC sequences used in the exemplification of the present invention

XX

SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.2e-243 Length: 2018

Score: 2453.00 Matches: 475

Percent Similarity: 84.63% Conservative: 59

Best Local Similarity: 75.28% Mismatches: 81

Query Match: 75.45% Indels: 16

DB: 3 Gaps: 6

US-10-025-145A-65 (1-618) x AAA38922 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15

Db 6 ATGGCTCTAGTTTCTACCGCACCGTTGGCTTCCAAATCATGCCTGCACAAATCGTTGATC 65

QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35

Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAAATTCACGCTCTAGGAATGAGTAGG 125

QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55

Db 126 CGAGGGAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACCGTTGTAACCGATGAT 185

QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75

Db 186 GGTGTACGAAGACGCATGGCGGATTTCCATTCCAAACCTCTGGGACGATGATGTACAG 245

QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95



Db 246 TCITTTA---CCAAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGCTGAGAAACTGATC 302

Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112

Db 303 GGGGAAGTAAAGAAC---ATGTTCAATTTCGATGTCATTAGAAGATGGAGAGTTAATGAGT 359

Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeuGlyIle 130

Db 360 CCGCTCAATGATCTCATTCACCGCCTTTGGATGTGCGACAGCCTTGAACGTTTGGGGATC 419

Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150

Db 420 CATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATGTTTACAGTTATTGGGGC 479

Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170

Db 480 GAAATGCGATCGGATCGGGAGGGAGAGTGTGTTACTGATCTGAACCTCAACTGCGGTTG 539

Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190

Db 540 GGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTTCAAAGCTTTC 599

Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAlaAsnIleGlnIleGluGlyGluIleArg 210

Db 600 AAAGGCCAAAATGGGCAGTTTTTCTGCTCTGAAAATATTTCAGACAGATGAAGAGATCAGA 659

Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230

Db 660 GCGGTTCTGAATTTATTCCGGGCTCCCTCATTTGCCTTTCCAGGGAGAAAAATTATGGAT 719

Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250

Db 720 GAGGCTGAAATCTTCTCTACCAATAATTAAAAAGAGCCCTGCAAAAGATTCCGGTCTCC 779

Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheHisThrAsnLeuPro 270

Db 780 AGT---CTTTCCGGAGAGATCGGGGACGTTTTTGGAAATATGGTTGGCACACATATTGCCG 836

Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290

Db 837 CGATTGGAAGCAAGGAATTACATCCCAAGTCTTTGGACAGGACACTGAGAACACGAAGTCA 896

Qy 291 -----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307

Db 897 TATGTGAAGAGCAAAAAACITTTTAGAACTCGCAAAATTTGGAGTTCAACATCTTTCAATCC 956

Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327

Db 957 TTACAAAAGAGGGAGTTAGAAAGTCTGGTCAGATGGTGGAAGAAGATCGGGTTTTCTCTGAG 1016

Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347

Db 1017 ATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTGGCTTCCTGTCATTGCGTTC 1076

Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367

Db 1077 GAGCCTCAACATTCTGGATTTCAGACTCGGCTTTGCCAAGACGTGTCATCTTATCACGGTT 1136

Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387

Db 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACA 1196

Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407

Db 1197 ATGAAGAGATGGGATCCGTCCTCGATAGATTGCTTCCAGAAATATATGAAAGGAGTGTAC 1256

Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427

Db 1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCGAGAGGAGGCTCAAGGCCGA 1316

Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447

Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTTCGTATATGCAAGAA 1376

Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1377 GCAAGGTGGATCGCCACTGGTTACTCTGCCCTCCTTTGATGAGTACTACGAGAATGGGAAA 1436

Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487

Db 1437 GTTAGCTGTGGTCATCGCATATCCGCATTTGCAACCCATTCTGACAAATGGACATCCCCCTTT 1496

Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507

Db 1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATTCAAAGCTTAACGACTTGGCATGTGCC 1556

Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527

Db 1557 ATCCTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGCTCGTGGAGAAGAA 1616

Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547

Db 1617 GCTTCCTCTATATCATGTTATATGAAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676

Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567

Db 1677 GATCATATCAACGCCATGATCAGTGACGTAAATCAAAGGATTAATTTGGGAACCTTCTCAA 1736

Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587

Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796

Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607

Db 1797 CATTACGGCTACAAATACCGAGACGGCTACAGCGTTTGCCCAACGTTGAAACGAAGAGTTTG 1856

Qy 608 ValMetArgThrValIleGluProValProLeu 618

Db 1857 GTCACGAGAAACCTCTCTGAATCTGTGCCTTTG 1889

RESULT 4

AAAF73372

ID AAF73372 standard; cDNA; 2018 BP.

XX AAF73372;

XX 30-APR-2001 (first entry)

DE Grand fir (-)-pinene synthase coding sequence SEQ ID NO: 3.

XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.

OS Abies grandis.

XX WO200107565-A2.

PN 01-FEB-2001.

PF 24-JUL-2000; 2000WO-US020264.

XX 26-JUL-1999; 99US-00360545.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Steele CL, Bohlmann J, Croteu RB, Phillips MA;

DR WPI; 2001-182782/18.

DR P-PSDB; AAB69371.

XX New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.

XX Claim 38; Page 108-110; 175pp; English.

XX The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.2e-243 Length: 2018  
Score: 2453.00 Matches: 475  
Percent Similarity: 84.63% Conservative: 59  
Best Local Similarity: 75.28% Mismatches: 81  
Query Match: 75.45% Indels: 16  
DB: 4 Gaps: 6  
US-10-025-145A-65 (1-618) x AAF73372 (1-2018)  
QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
Db 6 ATGGCTCTAGTTCTACCGCACCGTTGGCTTCCAATCATGCCTGCACAAATCGTTGATC 65  
QY 16 SerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAAATTCAGCTCTAGGAATGAGTAGG 125  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 126 CGAGGGAATCTATCACTCTCCATCAGCATGAGCTCTACCACCGTTGTAAACCGATGAT 185  
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75  
Db 186 GGTGTACGAAGACGCATGGCGGATTTCATCCATCAGCATGAGCTCTACCACCGTTGTAAACCGATGAT 245  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAAATCGTACCTGGAGCGTGTGAGAAACTGATC 302  
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTCGATGTCATTAGAGATGGAGAGTTAATGAGT 359  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130  
Db 360 CCGCTCAATGATCTCATTCACCGCTTTGGATTGTCGACAGCCTTGACGTTTGGGGATC 419  
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
Db 420 CATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATTACAGTTATTGGGGC 479  
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 480 GAAATGGCATCGGATCGGGAGGGAGAGTGTGTGTACTGATCTGAACTCAACTGCGTTG 539  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 540 GGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTCAAAGCTTTT 599  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
Db 600 AAAGGCCAAAATGGCAGTTTTCCTGCTCTGTAATAATATTCAGACAGATGAAGAGATCAGA 659  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 660 GCGGTTCTGAATTTATTCGGGCGCTCCCTCATTCGCTTCCAGGGGAGAAAAATTATGGAT 719  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 720 GAGGCTGAATCTTCTCTACCAAATATTTAAAGAGAGCCCTGCAAAAGATTCGGTCTCC 779

QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270  
Db 780 AGT---CTTTCGGGAGAGATCGGGGACGTTTTTGGAAATATGTTGGCACACATATTTGCCG 836  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290  
Db 837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTTTGGACAGGACACTGAGAACACGAAAGTCA 896  
QY 291 -----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307  
Db 897 TATGTGAAGAGCAAAAACCTTTTAGAACTCGCAAAATTGGAGTTCAACATCTTTCAATCC 956  
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327  
Db 957 TTACAAAAAGAGGGAGTTAGAAAAGTCTGGTCAGATGGTGGAAAGAAATCGGGTTTTTCTCTGAG 1016  
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
Db 1017 ATGACCTTCTGCCGACATCGTCCGTCAGTGAATACTACACTTTTGGCTTCTCGATTGCGTTC 1076  
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
Db 1077 GAGCCTCAACATTTCTGGATTCAGACTCGGCTTTGCCAAGACGCTGTCATCTTATCACGGTT 1136  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387  
Db 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACTCTTCACAGCGACA 1196  
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
Db 1197 ATGAAGAGATGGGATCCGTCCTCGATAGATTGCCTTCCAGAATATATGAAAGGAGTGTAC 1256  
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427  
Db 1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCAGAGGAGGCTCAAGGCCGA 1316  
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447  
Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTGTTATATGCAAGAA 1376  
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
Db 1377 GCAAGGTGGATCGCCACTGGTTACCTGCCCTCCTTTGATGAGTACTACGAGAATGGGAAA 1436  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487  
Db 1437 GTTAGCTGGTTCATCGCATATCCGCAATTGCAACCCATTTCTGACAAATGGACATCCCCCTT 1496  
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
Db 1497 CCTGATCATATCTCTCAAGGAAGTTGACTTCCCATCAAAGCTTAAACGCTTGGCATGTGCC 1556  
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527  
Db 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTACAAAGCGGACAGGGCTCGTGGAGAAGAA 1616  
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547  
Db 1617 GCTTCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676  
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567  
Db 1677 GATCATATCAACGCCATGATCAGTCAGTCGTAATCAAAGGATTAATTTGGGAACCTTCTCAA 1736  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587  
Db 1737 CCAGACATCAATGTTCCCATCTCGGCCAAGAAACATGCTTTTGGATCATCGCCAGAGCTTTC 1796  
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607  
Db 1797 CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAGAGTTTG 1856





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QY 402 TyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAla 421
Db 1273 TATATGAAGAAATCTACATGGCACTTACGAAGCCTTAACCTGACATGGCGGAGGCA 1332
QY 422 GluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPhe 441
Db 1333 GAGAAGACACAAGCCGAGACACGCTCAATTATGCTAGAAAGGCTTGGGAAGTTTATCTT 1392
QY 442 AspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGlu 461
Db 1393 GATTTCGTATACACAAGCAAGCAAGTGGATCGCCAGCGGTTATCTGCCAACTTTCGAGGAG 1452
QY 462 TyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu 481
Db 1453 TACTTAGAAGACGGAAGTTAGCTCTGCTCATCGTGCAGCGGCATGACACCCCTCCTG 1512
QY 482 ThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeu 501
Db 1513 ACATTGGACGTACCGCTTCCTGTATGACGTCTTGAAGGGAATAGATTTCATCGAGATT 1572
QY 502 AsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAsp 521
Db 1573 AATGATTGGCATCTTCCTTCCTTAGACTAAGAGGTGACACACGATGTACAAGGCAGAC 1632
QY 522 ArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeu 541
Db 1633 AGGGACCGGAGAGAAGCGTCAAGCATATCGTGTATCATGAAAGACAATCCCGGATTA 1692
QY 542 ThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeu 561
Db 1693 ACAGAGGAAGATGCTCTCAATCATATCAATGCCATGATCAACGACATAATCAAGAATTA 1752
QY 562 AsnTrpGluLeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPhe 581
Db 1753 AATTGGGAATCTTCAAACCCGATAGCAATATTCCAATGACTGCACGGAACATGCTTAT 1812
QY 582 AspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsn 601
Db 1813 GAGATAACGAGAGCTTTCACCAACTTTACAAATATAGAGATGGCTTCAGCGTTGCCACT 1872
QY 602 ValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1873 CAAGAAACGAAAAAGTTTGGTGAGGAGACGGTCTCTTGAACCACTGTCCTCTT 1923

RESULT 6
AAX08643
ID AAX08643 standard; cDNA; 2196 BP.
XX
AC AAX08643;
XX
DT 27-SEP-1999 (first entry)
XX
DE Myrcene synthase gene.
XX
KW Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;
KW defense; plant seed; oil; meal; ss.
XX
OS Abies grandis.
XX
FH Key Location/Qualifiers
FT CDS 69..1952
FT /tag= a
FT /product= "Myrcene synthase"
XX
PN WO9902030-A1.
XX
PD 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US014528.
XX
PR 11-JUL-1997; 97US-0052249P.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
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XX Bohlmann J, Steele CL, Croteau RB;
PI WPI; 1999-120396/10.
XX P-PSDB; AAW85700.
DR
XX
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
PT fir (Abies grandis), used to provide plants with modified production of
PT monoterpenes, e.g. myrcene, limonene or pinene.
XX
PS Claim 9; Page 69-72; 121pp; English.
XX
CC Nucleotide sequences encoding myrcene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by myrcene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,01e-217 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 2 Gaps: 7

US-10-025-145A-65 (1-618) x AAX08643 (1-2196)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGGTTTCTATCTCACCGTTGGCTTCGAATCTTGCTCGCAAGTCGTTGATC 128
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCAATTCAATGAACATAAGCCCTCCCTATAGAACAATCCCAATCTTGGAAATCGGTAGG 188
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGGAAATCTGTACGCTTCCATGAGCATCAGTTTGGCCACCGCTGCACCTGATGAT 248
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGTACAAAGACGCATAGGTGACTACCATTCCAATATCTGGGACGATGATTTCATACAG 308
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA---TCAACGCCTTATGGGAACCCCTCTTACCAGGAACGTGCTGAGAGATTAAAT 365
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 366 GTGGAGGTAAAGAAGATA---TTCATTCATGTACCTGGATGATGGAAGATTAAATGAGT 422
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGGATA 482
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAGAACGAGATAACATCAGCTCTGGATTATGTTTCCGTTACTGGGAG 542
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACCGCATTTGGATGTGGGAGACACAGTATTGTTACTGATCTCAACTCAACTGCGTTG 602
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
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CC hormones and bile acids, as photoreceptors and as co-factor side chains.  
CC Some synthases with little or no catalytic activity (and nucleic acids  
CC encoding them) are used as controls in the analysis of products formed by  
CC enzymatic synthesis; as nutrient supplements; for affinity purification  
CC of isoprenoids; or to develop immunological reagents or nucleic acids for  
CC monitoring expression of terpene synthase or inheritance of the gene in  
CC plant breeding programs. The new synthases may produce novel terpene  
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.01e-217 Length: 2196  
Score: 2200.50 Matches: 427  
Percent Similarity: 80.38% Conservative: 77  
Best Local Similarity: 68.10% Mismatches: 106  
Query Match: 67.69% Indels: 17  
DB: 3 Gaps: 7

US-10-025-145A-65 (1-618) x AAA38927 (1-2196)

QY	1	MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu-----	15
Db	69	ATGGCTCTGGTTCTATCTCACCGTTGGCTCGAAATCTTGCCCTGGCAAGTCGTTGATC	128
QY	16	SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg	35
Db	129	AGTTCAATTCAATGAACATAAGCCTCCCTATAGAACAAATCCCAAATCTTGAATGCGTAGG	188
QY	36	ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp	55
Db	189	CGAGGAAATCTGTCACGCCTTCCATGAGCATCAGTTTGGCCACCGCTGCACCTGATGAT	248
QY	56	SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTirpAspAspPheIleGln	75
Db	249	GGTGTAACAAGACGCATAGGTGACTACCAATCCAAATCTGGACGATGATTCATACAG	308
QY	76	SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle	95
Db	309	TCTCTA---TCAACGCCTTATGGGAAACCCCTCTTACCAGGAACGTGCTGAGAGATTAAT	365
QY	96	GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly-----	112
Db	366	GTGGAGGTAAAGAAGATA--TTCAATTCAATGTACCTGGATGATGGAAGATTAAATGAGT	422
QY	113	-----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle	130
Db	423	TCCTTTAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGAACGTTTGGGGATA	482
QY	131	AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn	150
Db	483	GCTAGACATTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTCCGTTACTGGGAG	542
QY	151	GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu	170
Db	543	GAACAACGGCAATTGGATGTGGAGAGACAGTATTGTTACTGATCTCAACTCAACTGCGTTG	602
QY	171	GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValphe	190
Db	603	GGGTTTCGAACTCTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAAAGCTTTT	662
QY	191	LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg	210
Db	663	CAAGATCAAAATGGACAGTTTGTATGCTCCCGCGT--CAGACAGAGGGTGAGATCAGA	719
QY	211	GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp	230
Db	720	AGCGTCTTAACTTATATCGGGCTTCCCTCATGCTCCCTGGTGAGAAAGTTATGGAA	779
QY	231	GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer	250
Db	780	GAAGCTGAAATCTTCTCCACAAGATATTTGAAAGAAGCTCTACAAAAGATTCAGTCTCC	839

QY	251	SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro	270
Db	840	GCT---CTTTCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCACACAAATTTGCCA	896
QY	271	ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn	287
Db	897	AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAGTCGATGGCTCAAT	956
QY	288	LysAsnAlaAlaGluLysLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer	307
Db	957	AAAAATGCTGGGAAGAAGCTTTTAGAACTTGCAAAATTTGGAGTTCAATATATTAACTCC	1016
QY	308	LeuGlnGluArgGluLeuLysHisValSerArgTirpLysAspSerGlySerProGlu	327
Db	1017	TTACAACAAAAGGAATTACAATATCTTTTGAGATGGTGGAAAGAGTCGGATTTGCCTAAA	1076
QY	328	MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe	347
Db	1077	TTGACATTTGCTCGGCATCGTTCATGTGGAATCTACACTTTGGCCTCTTGTATTGCCATT	1136
QY	348	GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal	367
Db	1137	GACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCTATCTTGTACAGTT	1196
QY	368	LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr	387
Db	1197	TTGGACGATATTTACGACACTTTTGGAACGATTGACGAGCTTGAACTCTTCACATCTGCA	1256
QY	388	IleLysArgTirpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr	407
Db	1257	ATTAAGAGATGGAATTCATCAGAGATAGAAACACCTTCCAGAAATATATGAAATGTGTATC	1316
QY	408	MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg	427
Db	1317	ATGGTCGTGTTGAAACTGTAAATGAACTGACACGAGGCGGAGAACTCAAGGGAGA	1376
QY	428	AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu	447
Db	1377	AACACTCTCAACTATGTTTCGAAGGCTTGGAGGCTTATTTTGATTATATATGGAAGAA	1436
QY	448	AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys	467
Db	1437	GCAAAATGGATCTCTAATGGTTATCTGCCAATGTTTGAAGAGTACCATGAGAATGGGAAA	1496
QY	468	ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe	487
Db	1497	GTGAGCTCTGCATATCGCGTAGCAACATTTGCAACCCATCCTCACTTTGAATGCATGGCTT	1556
QY	488	ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle	507
Db	1557	CCTGATTACATCTTGAAGGGAATTGATTTCCATCCAGTTTCAATGATTTGGCATCGTCC	1616
QY	508	IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu	527
Db	1617	TTCCCTTCGGCTACGAGGTGACACACGCTGCTACAAGCCGATAGGGATCGTGGTGAAGAA	1676
QY	528	AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu	547
Db	1677	GCTTCGTGTATATCATGTTATATGAAGACAAATCCTGGATCAACCGAAGAAGATGCCCTC	1736
QY	548	AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys	567
Db	1737	AATCATATCAATGCCATGGTCAATGACATAATCAAGAATTAATTTGGGAACCTTCTAAGA	1796
QY	568	ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp	587
Db	1797	TCCAACGACAATATTTCCAATGCTGGCCAAAGAAACATGCTTTTGACATAACAAGAGCTCTC	1856
QY	588	HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu	607
Db	1857	CACCATCTCTACATATATCGAGATGGCTTTAGTGTTCGCCAACACAGGAAACAAAAAATTG	1916

QY 608 ValMetArgThrValIleGlu 614  
Db 1917 GTTATGGAACACTCCTTGAA 1937

RESULT 8  
AAF73371  
ID AAF73371 standard; cDNA; 2196 BP.  
XX AC  
XX AAF73371;  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir myrcene synthase coding sequence SEQ ID NO: 1.  
XX  
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX  
OS Abies grandis.  
XX  
PN WO200107565-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
XX  
DR WPI; 2001-182782/18.  
DR P-PSDB; AAB69370.  
XX  
PT New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
PS Claim 28; Page 103-106; 175pp; English.  
XX

The present invention provides the protein and coding sequences of  
monoterpene synthases from the grand fir. These include (-)-camphene  
synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
and pinene synthase. The sequences can be used to produce transgenic  
plants expressing high levels of the enzymes, resulting in levels which  
are useful in protecting against and treating cancers, and to confer  
insect resistance on plants

XX  
SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 2.01e-217 Length: 2196  
Score: 2200.50 Matches: 427  
Percent Similarity: 80.38% Conservative: 77  
Best Local Similarity: 58.10% Mismatches: 106  
Query Match: 67.69% Indels: 17  
DB: 4 Gaps: 7

US-10-025-145A-65 (1-618) x AAF73371 (1-2196)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
Db 69 ATGGCTCTGGTTTCTATCTCACCGTTGGCTTCGAAATCTTGCTGCGCAAGTCGTTGATC 128

QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
Db 129 AGTTCAATTCAATGAACATAAGCCTCCCTATAGAACAAATCCCAAATCTTGAATCGGTAGG 188

QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 189 CGAGGGAAATCTGTACGCCTTCCATGAGCATCAGTTTGGCCACCGCTGCACCTGATGAT 248

QY 56 SerValGlnArgValGlyAsnTyrHisSerAsnLeuTirAspAspPheIleGln 75  
Db 249 GGTGTACAAAGACGCATAGGTACTACCATTCCAATATCTGGGACGATGATTCATACAG 308

QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 309 TCTCTA---TCAACGCCCTTATGGGAAACCCCTCTTACCAGGAACGTCTGAGAGATTAATT 365

QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 366 GTGGAGGTAAAGAAAGATA--TTCAATTCAATGTACCTGGATGATGGAAGATTAATGAGT 422

QY 113 -----AsnAspLeuLeuGlnArgLeuLeuLeuValAspValGluArgLeuGlyIle 130  
Db 423 TCCTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTTGGGGATA 482

QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTirAsn 150  
Db 483 GCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTCCGTTACTGGGAG 542

QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 543 GAAAACGGCATTTGGATGTGGGAGAGACAGTATTGTTACTGATCTCAACTCAACTGCGTTG 602

QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 603 GGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 662

QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
Db 663 CAAGATCAAAATGGACAGTTTGTATGCTCCCCCGGT---CAGACAGAGGGTGAGATCAGA 719

QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 720 AGCGTTCTTAACCTATATCGGGCTTCCTCATTCCTTCCCTGGTGAGAAAGTTATGGAA 779

QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 780 GAAGCTGAAATCTTCTCCACAAGATATTGAAAGAAGCTCTACAAAAGATTCCAGTCTCC 839

QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTirHisThrAsnLeuPro 270  
Db 840 GCT--CTTTCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCACACAAATTTGCCA 896

QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287  
Db 897 AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAGTGCATGGCTCAAT 956

QY 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307  
Db 957 AAAAATGCTGGGAAGAAGCTTTTAGAACTTGCAAAATTTGGAGTTTCAATATATTTAACTCC 1016

QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTirPirLysAspSerGlySerProGlu 327  
Db 1017 TTACAACAAAAGGAATTACAATATCTTTGAGATGGTGGAAAGAGTCGGATTTGCCTAAA 1076

QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
Db 1077 TTGACATTTGCTCGGCATCGTCATGTGGAATTTCTACACTTTGGCCTCTTGTATTGCCATT 1136

QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
Db 1137 GACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCTATCTTGTACAGTT 1196

QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387  
Db 1197 TTGGACGATATTTCGACACCTTTTGGAACGATTGACGAGCTTGAACTCTTCACATCTGCA 1256

QY 388 IleLysArgTirPirAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
Db 1257 ATTAAGAGATGGAATTTCATCAGATAGAAACACCTTCCAGAATATATGAAATGTGTGTAC 1316







Db 591 GGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAAAGCTTTT 650  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
Db 651 CAAGATCAAAATGGACAGTTTGTATGCTCCCGCGT--CAGACAGAGGGTGAGATCAGA 707  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 708 AGCGTTCCTTAACCTATATCGGGCTTCCTCATGTCCTTCCCTGGTGAGAAAGTTATGGAA 767  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 768 GAAGCTGAAATCTCTCCACAAGATATTTGAAAGAAGCTCTACAAAAGATTCCAGTCTCC 827  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270  
Db 828 GCT---CTTTCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCACACAAAATTGCCA 884  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287  
Db 885 AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAGTGGCTCAAT 944  
QY 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307  
Db 945 AAAAATGCTGGGAAGAAGCTTTTAGAACTTGC AAAATTGGAGTTCAATATATTAACTCC 1004  
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327  
Db 1005 TTACAACAAAAGGAATTACAATATCTTTTGAGATGGTGGAAGAGTCGGATTTGCCTAAA 1064  
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
Db 1065 TTGACATTTCGCGCATCGTCATGTGGAATTTCTACACTTTGGCCTCTTGTATGGCATT 1124  
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
Db 1125 GACCCAAAACATTTCTGATTTCAGACTAGGCTTCGCCAAAATGTGTCACTCTTCACAGTT 1184  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387  
Db 1185 TTGGACGATATTTACGACACTTTTGGAAACGATTGACGAGCTTGAACCTCTTCACATCTGCA 1244  
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
Db 1245 ATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGAAATATATGAAATGTGTGTAC 1304  
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427  
Db 1305 ATGGTCGTGTTTGAACTGTAAATGAACTGACACGAGAGGCGGAGAGACTCAAGGGAGA 1364  
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447  
Db 1365 AACACTCTCAACTATGTTCGAAAGGCTTGGGAGGCTTATTTTGATTTCATATATGGAAGAA 1424  
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
Db 1425 GCAAAATGGATCTCTAATGGTTATCTGCCAACGTTTGAAGAGTACCATGAGAATGGGAAA 1484  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnPheLeuThrLeuAspIleProPhe 487  
Db 1485 GTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCTCTCACTTTGAATGCTGGCTT 1544  
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
Db 1545 CCTGATTACATCTTGAGGGAATTGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1604  
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527  
Db 1605 TTCCTTCGGCTACGAGGTGACACACGCTGCTACAAAGCCGATAGGGATCGTGTGTGAAGAA 1664  
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547

Db 1665 GCTTCGTGTATATCATGTTATATGAAGACAAATCCTGGATCAACCCGAAGAATGCCCTC 1724  
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567  
Db 1725 AATCATATCAATGCCATGGTCAATGACATAATCAAAGAATTAAATTGGGAACCTTCTAAGA 1784  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587  
Db 1785 TCCAACGACAATATTCGAATGCTGGCCAAGAAACATGCTTTTGACATAACAAGAGCTCTC 1844  
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607  
Db 1845 CACCATCTCTACATATATCGAGATGCGCTTAGTGTGCCAACACAGGAAACAAAAAATTG 1904  
QY 608 ValMetArgThrValIleGlu 614  
Db 1905 GTTATGGAAACACTCCTTGAA 1925  
RESULT 10  
AAF73391  
ID AAF73391 standard; cDNA; 2205 BP.  
XX  
AC AAF73391;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 31.  
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.  
XX Abies grandis.  
OS  
XX WO200107565-A2.  
PN  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
PI WPI; 2001-182782/18.  
XX P-PSDB; AAB69380.  
DR  
DR New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
PS Example 3; Page 135-137; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 4.13e-217 Length: 2205  
Score: 2197.50 Matches: 427  
Percent Similarity: 80.38% Conservative: 77  
Best Local Similarity: 68.10% Mismatches: 106  
Query Match: 67.59% Indels: 17  
DB: 4 7

US-10-025-145A-65 (1-618) x AAF73391 (1-2205)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15

Db 57 ATGGCTCTGTTTCTATCTCACCGTTGGCTTCGAATCTTGCCCTGCGCAAGTCGTTGATC 116

QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35

Db 117 AGTTCAATTCAATGACATGAATAGCCTCCCTATAGAACAAATCCCAAATCTTGGAATGCGTAGG 176

QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55

Db 177 CGAGGGAAATCTGTACGCTTCCATGAGCAATCAGTTTGGCCACCGCTGCACCTGATGAT 236

QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIleGln 75

Db 237 GGTGTACAAAGACCGCATAGGTGACTACCATCTCCAATATCTGGACGATGATTCATACAG 296

QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95

Db 297 TCTCTA--TCAACGCATTATGGGAAACCTCTTACCAGGAACGTGCTGAGAGATTAAAT 353

QY 96 GlyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112

Db 354 GTGGAGGTAAAGAGATA--TTCAATTCAATGTACCTGGATGATGGAAGATTAAATGAGT 410

QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspValGluArgLeuGlyIle 130

Db 411 TCCTTTAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGAACGTTTGGGGATA 470

QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150

Db 471 GCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTCCGTTACTGGGAG 530

QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170

Db 531 GAAACCGCATTCGATGTGGGAGAGACAGTATTGTACTGATCTCAACTCAACTCGCTTG 590

QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190

Db 591 GGGTTTCGAACCTCTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAAGCTTTT 650

QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210

Db 651 CAAGATCAAAATGGACAGTTTGTATGCTCCCCCGGT---CAGACAGAGGGTGAGATCAGA 707

QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230

Db 708 AGCGTTCTTAACTTATATCGGGCTTCCCTCAATGCGCTTCCCTGGTGAGAAAGTTATGGAA 767

QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250

Db 768 GAAGCTGAAATCTTCTCCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCACACAATTTGCCA 884

QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270

Db 828 GCT---CTTTCAAGAGAGATAAAGTTTGTATGGAATATGGCTGGCACACAATTTGCCA 884

QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287

Db 885 AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAGTCGATGGCTCAAT 944

QY 288 LysAsnAlaAlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307

Db 945 AAAAATGCTGGGAAGAGCTTTTAGAACTTGCAAAATTTGGAGTTCAATATATTAACTCC 1004

QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327

Db 1005 TTACAACAAGAAATTACAATATCTTTTGAGATGGTGGAAAGAGTCGGATTTGCCTAAA 1064

QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347

Db 1065 TTGACATTTGCTCGGCATCGTCATGTGGAATCTACACTTTGGCCTCTTGTATTGCCATT 1124

QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367

Db 1125 GACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCACTTTGTACAGTT 1184

QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387

Db 1185 TTGGACGATATTACACACATTTTGGAACGATTGACGAGCTTGAACCTCTTCACATCTGCA 1244

QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407

Db 1245 ATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGAATATATGAAATGTGTGTAC 1304

QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427

Db 1305 ATGGTCGTGTTTGAACCTGTAATGAACCTGACACGAGAGCGGAGAACTCAAGGGAGA 1364

QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnGlu 447

Db 1365 AACACTCTCAACTATGTTCGAAAGGCTTGGGAGGCTTATTTTGATTATATATATGAAGAA 1424

QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1425 GCAAAATGGATCTCTAATGGTTATCTGCCAACGTTTGAAGAGTACCATGAGAAATGGGAAA 1484

QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProphe 487

Db 1485 GTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCCTCACTTTGAATGCATGGCTT 1544

QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507

Db 1545 CCTGATTACATCTTGAAGGGAATTGATTTTCCATCCAGGTTCAATGATTGGCATCGTCC 1604

QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527

Db 1605 TTCCTTCGGCTAGGAGGTGACACACGCTGCTACAAGGCCGATAGGGATCGTGGTGAAGAA 1664

QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547

Db 1665 GCTTCGTGTATATCATGTTTATATGAAAGACAATCCTGGATCAACCGAAGAAGATGCCCTC 1724

QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567

Db 1725 AATCATATCAATGCCATGGTCAATGACATAATCAAAGAATTAAATTTGGAACTTCTAAGA 1784

QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587

Db 1785 TCCAACGACATATTTCCAATGCTGGCCCAAGAAACATGCTTTTGACATAACAAGAGCTCTC 1844

QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607

Db 1845 CACCATCTCTACATATATCGAGATGGCTTTAGTGTGTTGCCAACAGGAAACAAAAAATTG 1904

QY 608 ValMetArgThrValIleGlu 614

Db 1905 GTTATGGAAACACTCCTTGAA 1925

RESULT 11

AAF73421

ID AAF73421 standard; cDNA; 1890 BP.

XX

AC AAF73421;

XX

DT 30-APR-2001 (first entry)

XX

DE Grand fir monoterpene synthase coding sequence SEQ ID NO: 77.

XX

KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;

KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;

KW terpinolene synthase; insect resistance; nutrition; ss.

OS Abies grandis.

XX WO200107565-A2.  
PN  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-US020264.  
XX  
PR 26-JUL-1999; 99US-00360545.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
XX Steele CL, Bohlmann J, Croteu RB, Phillips MA;  
PI  
XX WPI; 2001-182782/18.  
DR P-PSDB; AAB69393.  
DR  
XX  
XX New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.  
XX  
XX  
PS Claim 18; Page 163-165; 175pp; English.  
XX  
CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants  
XX  
SQ Sequence 1890 BP; 550 A; 381 C; 441 G; 518 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.11e-211 Length: 1890  
Score: 2137.00 Matches: 427  
Percent Similarity: 78.86% Conservative: 73  
Best Local Similarity: 67.35% Mismatches: 114  
Query Match: 65.73% Indels: 20  
DB: 4 Gaps: 9  
  
US-10-025-145A-65 (1-618) x AAF73421 (1-1890)  
  
Qy 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeuSer----- 16  
Db 1 ATGGCTCTGTTCATCTTGCCCTTGTCCTCCAAATCGGTCCTGCACAAATCGTGGATC 60  
  
Qy 17 ---SerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
Db 61 GTTTCVACTTATGAGCATAAGGCTATCAGTAGAACAAATCCCAATCTTGATTCGGTGGG 120  
  
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 121 CGAGGGAATCTGTGACACATTCCTCGAGAATGAGTTTGAGCACCGCAGTCTCTGATGAT 180  
  
Qy 56 ---SerValGlnArgValGlyAsnTyrHisSerAsnLeuTrpAspPheIle 74  
Db 181 CATGGTGTAACAAAGACGCATAGTCGAGTTTCATTCCAAATCTGTGGACGACGATTTCATA 240  
  
Qy 75 GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu 94  
Db 241 CAATCTCTA---TCAACGCCTTATGGGCACCTTCATACCCGTGAACGTGCTGATAGACTT 297  
  
Qy 95 IleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 298 ATTTGTGAAGTAAGGGTATA---TTCACCTTCAATTCAGCGGAAGATGGAGAACTAATC 354  
  
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129  
Db 355 ACTCCCTCAATGATCTCATTCACGCCCTTTAATGGTCGATAACGTTGAACGTTTAGGG 414  
  
Qy 130 IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrp 149  
Db

Db 415 ATTGATAGACATTTCAAAAATGAGATAAAAGCAGCACTAGACTATGTTTACAGTTATTGG 474  
Qy 150 AsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169  
Db 475 AACGAAAAAGGCATGGCAGTGGAAGTGATAGTGGTGTGCTGATCTCAACTCAACTGCC 534  
Qy 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnVal 189  
Db 535 CTGGGGTTTCGAATTCCTCGACTACACGATACAGTGTTCCTTCAGATGTGTGGAACAC 594  
Qy 190 PheLysAsp-----LysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGly 207  
Db 595 TTCAAAGAGGAGAGAGAGAGGGGCGAGTTTGTATGTTCGGCC---ATCCAAACAGAGGAA 651  
Qy 208 GluIleArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLys 227  
Db 652 GAGATAAAAGCGTTCTGAATTTATTTCGGGCCTCCCTCATTTGCCCTTCTCTGGGAGAAA 711  
Qy 228 ValMetAspGluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIle 247  
Db 712 GTTATGGAAGAGGCTGAAATCTTCTCTAAAAATATATTTAAAGAGCCTTACAAAATATT 771  
Qy 248 ProAlaSerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThr 267  
Db 772 GCTGTCTCCAGT---CTTTCACGAGAGATAGAGTACGTTCTTGAGGATGGTTGGCAACA 828  
Qy 268 AsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsn 287  
Db 829 AATATGCCAAGATTGGAAACAAGGAACACTACATCGATGTATTGGGAGAGAACGATCGTAT 888  
Qy 288 LysAsnAla-----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIle 304  
Db 889 GAGACGTTATATATGAACATGGAGAAACTTTTAGAAATTGCAAAATTGGAGTTCAATATT 948  
Qy 305 PheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGly 324  
Db 949 TTTCACTCTCTTACAACAGAGAGAGCTAAAAGACCTCTCCAGATGGTGGAAAGATTTCGGGT 1008  
Qy 325 SerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCys 344  
Db 1009 TTCTCTCACCTGACATTTTCTCGGCATCGTCATGTGGAATCTACGCTCTGGCATCTTGC 1068  
Qy 345 IleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeu 364  
Db 1069 ATTGAAACTGATCGCAACACATTCGGGATTCAGACTCGGCTTTGCCAAAATGTGTCACTTT 1128  
Qy 365 IleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPhe 384  
Db 1129 ATCACGGTTTGGACGATATATACGACACCTTTTGGAAACAATGGAGAGCTGGAACTCTTC 1188  
Qy 385 ThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLys 404  
Db 1189 ACTGCACCATTTAAGAGATGGGATCCGTCTGCCACAGATTTGCTTCAGAGTATATGAAA 1248  
Qy 405 GlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAla 424  
Db 1249 GGGTTGTACATGGTGGTTTACGAAACCGTAAATGAAATTGCTCGAGAGGCAGACAAGTCT 1308  
Qy 425 GlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyr 444  
Db 1309 CAAGGCGGAGAGACGCTCAACGATGCTCGACGAGCTTGGGAGGCCCTATCTTGAATTCGAT 1368  
Qy 445 MetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGlu 464  
Db 1369 ATGAAAGAAGCTGAGTGGATCTCCAGTGGTTATCTGCCAACGTTTGAGGAGTACATGGAG 1428  
Qy 465 AsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAsp 484  
Db 1429 ACCAGCAAAGTTAGTTTTGGTTATCGCATATTTCGCATTGGCAACCCCATCCTCACTATGGAT 1488  
Qy 485 IleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeu 504  
Db 1489 GTTCCCTTACTCACCCACATCTCGAGGAAATAGACTTTCCATTGAGGTTTAATGACTTA 1548







QY 296 GluLeuAlaLysLeuGluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHis 315  
Db :::  
977 AAACCTTGCAAAATGGAGTTTAATATCTTTCACTCTTGCACAGAAAGAGTTGCAATAT 1036

QY 316 ValSerArgTrpTrpLysAspSerGlySerProGluMetThrPheCysArgHisArgHis 335  
Db :::  
1037 ATCTCTAGATGGTGAAGATTTCGTGTTCACTCTCATCTGACTTTTACTCGACACCGTCAC 1096

QY 336 ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArg 355  
Db :::  
1097 GTGGAATACTACACAATGGCATCTTGCAATTTCTATGGAGCCGAAACACTCCGCTTTCAGA 1156

QY 356 LeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetTyrAspValPhe 375  
Db :::  
1157 TTGGGGTTTGTCAAACATGTCTATCTTCTTAACAGTTCTGGATGATATGACACTTTT 1216

QY 376 GlyThrValAspGluLeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAla 395  
Db :::  
1217 GGAACACTGGACCAACTCCAACCTTTTACGACTGCCCTTAAAGAGATGGGATTTGTCAGAG 1276

QY 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn 415  
Db :::  
1277 ACAAGTGTCTCCAGAATATATGAAGCGAGTGTACATGGACTTGTATCAATGCTTAAT 1336

QY 416 GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln 435  
Db :::  
1337 GAATTGGCGCAAGAGGCTGAGAAGACTCAAGGCAGAGATACGCTCAACTATATTCGCAAT 1396

QY 436 AlaTipGluAlaCysPheAspSerTyrMetGlnGluAlaLysTipIleAlaThrGlyTyr 455  
Db :::  
1397 GCTTATGAGTCTCATTTTGATTTCGTTTATGCAGGAAGCAAAATGGATCTCAAGTGGTTAT 1456

QY 456 LeuProThrPheGluGluTyrLeuGluAsnGlnGlyLysValSerSerAlaHisArgProCys 475  
Db :::  
1457 CTCCCAACGTTGAGGAGTACTTTGAAGATGGGAAAGTTAGTTCCGGTTCTCGCACAGCC 1516

QY 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495  
Db :::  
1517 ACTTTACACCCATACTCACCTTGGATGTACCACTTCCTAATTACATACTGCAAGAAAT 1576

QY 496 AspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515  
Db :::  
1577 GATTATCCATCTAGGTTCAATGACTTGGCTTCGTCCCTCCTTCGGCTACGTGGTGACACG 1636

QY 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535  
Db :::  
1637 CGCTGTACTAAGCGGATAGGGCTCGTGAGAGAAGAGCTTCAGCTATATCGTGTATATG 1696

QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555  
Db :::  
1697 AAAGACCATCTGGATCAACAGAGGAAGATGCTCTCAATCATATCAACGTCATGATCAGT 1756

QY 556 AspAlaIleArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThr 575  
Db :::  
1757 GATGCAATCAGAGAATTAAATTGGAGCTTCTCAGACCAGATAGCAAAAGTCCCATCTCT 1816

QY 576 SerLysLysHisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAsp 595  
Db :::  
1817 TCCAAGAAACATGCTTTTGACATCACAGAGCTTTCCATCACCTCTACAAGTACCCGAGAT 1876

QY 596 GlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGluPro 615  
Db :::  
1877 GGTTACACTGTTGCGAGTAGTGAACAAGAAATTTGGTGATGAAACAGTTCTTTGAACCT 1936

QY 616 ValProLeu 618  
Db :::::  
1937 GTGGCAATG 1945

RESULT 13  
AAX08645  
ID AAX08645 standard; cDNA; 2089 BP.  
XX

AC AAX08645;  
XX  
DT 27-SEP-1999 (first entry)  
XX  
DE Limonene synthase gene.  
XX  
KW Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.  
XX  
OS Abies grandis.  
XX  
FH Key Location/Qualifiers  
FT CDS 73..1986  
FT /\*tag= a  
FT /product= "Limonene synthase"  
XX  
PN WO9902030-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98WO-US014528.  
XX  
PR 11-JUL-1997; 97US-0052249P.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
XX Bohlmann J, Steele CL, Croteau RB;  
PI  
XX  
DR WPI; 1999-120396/10.  
DR P-PSDB; AAW85702.  
XX  
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. myrcene, limonene or pinene.  
XX  
PS Claim 11; Page 79-82; 121pp; English.  
XX  
CC Nucleotide sequences encoding myrcene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by myrcene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal  
XX  
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 6.08e-200 Length: 2089  
Score: 2031.50 Matches: 409  
Percent Similarity: 76.67% Conservative: 84  
Best Local Similarity: 63.61% Mismatches: 119  
Query Match: 62.49% Indels: 31  
DB: 2 Gaps: 14

US-10-025-145A-65 (1-618) x AAX08645 (1-2089)

QY 1 MetAlaLeuSerIleThrProLeu---ValSerArgSerCys----- 14  
Db 73 ATGGCTCTCCTTCTATCGTATCTTTGCAGGTTCCCAATCTCGGGCTGAAATCGTTG 132  
QY 15 LeuSerSerHisGluIleLysAlaLeu-----ArgArgThrIleProThrLeuGly 32  
Db 133 ATCATGTCAGCAATGTGCAGAGAGGCTCTCTGTATCTCTACAGCAGTCCCAACTCAGA 192  
QY 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52  
Db 193 ATCGGTAGGGCAGAGAAAGCTCTGGTC-----ATCAACATGAAATGACCACCTGTATCC 246  
QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnTyrHisSerAsn 67

Db 247 CATCGTATGATAATGGTGGTGTACTGCAAAAGACGCATAGCCGATCATATCCCAAC 306  
QY 68 LeuTrpAspAspPheIleGlnSerLeuIleSerThrProTyrGlyAlaProAspTyr 87  
Db 307 CTGTGGGAAGATGATTTTCATACATCATG---TCCTCACCTTATGGGGGATCTTCGTAC 363  
QY 88 ArgGluArgAlaAspArgLeuIleGlyGluValLysAspIleMetPheAsnPhe----- 105  
Db 364 AGTGAACCTGCTGAGACAGTCGTTGAGGAAGTAAAGAG---ATGTTCAATTCATAACCA 420  
QY 106 -----LysSerLeuGluAspGlyGlyAsnAspLeuLeuGlnArgLeuLeuValAsp 123  
Db 421 AATAATAGAGAATTATTTGGTTCCTCAAAATGATCTCTTACACGCTTTGGATGGTGGAT 480  
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThrAlaLeuAsp 143  
Db 481 AGCAATTGAACGCTCTGGGATAGATAGACATTTCCAAAATGAGATAAGAGTAGCCCTCGAT 540  
QY 144 TyrValAsnSerTyrTrpAsnGluLys---GlyIleGlyCysGlyArgGluSerValVal 162  
Db 541 TATGTTTACAGTTATTGGGAAGGAAGGAAGGCATTGGGTGTGGCAGAGATTCTACTTTT 600  
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrVal 182  
Db 601 CCTGATCTCAACTCGACTGCCTTGGCGCTTCGAACTCTTCGACTGCGAGGATACAATGTG 660  
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202  
Db 661 TCTTCAGATGCTGGAATACTTCAAAAGATGAAAAGGGGCATTTTGCCTGCCCTGCA--- 717  
QY 203 IleGlnIleGlyGluIle---ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221  
Db 718 ATCCTAACCGAGGACAGATCACTAGAAAGTCTTCTAAATTATATCGGCTTCCCTGGTC 777  
QY 222 AlaPheProGlyGluLysValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241  
Db 778 GCCTTTCCCCGGGAGAAAGTTATGGAAGAGGCTGAAATCTTCTCGGCATCTTATTGAAA 837  
QY 242 GluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspValLeu 261  
Db 838 AAAGTCTTTACAAAAGATTCCGGTCTCCAAAT---CTTTCAGGAGAGATAGAATATGTTTG 894  
QY 262 GluTyrGlyTrpHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPhe 281  
Db 895 GAATATGGTTGGCACACGAATTTGCCGAGATTGGAAGCAAGAAATATATCGAGGCTCTAC 954  
QY 282 -----GlyGlnHisThrLysAsnLysAsnAla-----AlaGluLysLeuLeu 295  
Db 955 GAGCAGAGCGGCTATGAAAGCTTAAACGAGATGCCATATATGAACATGAAGAAGCTTTTA 1014  
QY 296 GluLeuAlaLysLeuGluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHis 315  
Db 1015 CAACCTTGCAAAATGGAGTTCAATATCTTTCACTCTTTGCAACTAAGAGAGTTACAATCT 1074  
QY 316 ValSerArgTrpTrpLysAspSerGlySerProGluMetThrPheCysArgHisArgHis 335  
Db 1075 ATCTCCAGATGGTGGAAAGAAATCAGGTTTCGTCTCAACTGACTTTTACACGGCATCGTCAC 1134  
QY 336 ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArg 355  
Db 1135 GTGGAATACTACTATGGCATCTTGCATTTCTATGTTGCCAAAACATTCAGCTTTCAGA 1194  
QY 356 LeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetTyrAspValPhe 375  
Db 1195 ATGGAGTTTGTCAAAGTGTGTCTCTTGTAAAGTCTTCGATGATATATATGACACTTTT 1254  
QY 376 GlyThrValAspGluLeuGluPheThrAlaThrIleLysArgTrpAspProSerAla 395  
Db 1255 GGAACAATGAACGAACTCCAACTTTTACGGATGCAATTAAGAGATGGGATTTGTCAACG 1314  
QY 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn 415

Db 1315 ACAAGGTGGCTTCCAGAAATATATGAAAGGAGTGATACATGGACTTGTTATCAATGCATTAAT 1374  
QY 416 GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln 435  
Db 1375 GAAATGGTGAAGAGGCTGAGAAGACTCAAGGCCGAGATATGCTCAACTATATTCAAAAT 1434  
QY 436 AlaTrpGluAlaCysPheAspSerTyrMetGlnGlnAlaLysTrpIleAlaThrGlyTyr 455  
Db 1435 GCTTGGGAAGCCCTATTTGATACCTTTATGCAAGAGCAAAAGTGGATCTCCAGCAGTTAT 1494  
QY 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475  
Db 1495 CTCCCAACGTTTGAGGAGTACTTGAAGAATGCAAAAGTTAGTTCTGGTCTCGCATAGCC 1554  
QY 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495  
Db 1555 ACATTACAACCCATTCTCACTTTTGGATGTACCCTTCCTGATTACATACTGCAAGAAAT 1614  
QY 496 AspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515  
Db 1615 GATTATCCATCCAGATTCAATGAGTTAGTTCGTCCATCCTTCGACTACGAGGTGACACG 1674  
QY 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535  
Db 1675 CGCTGCTACAAGCGGATAGGGCCGTCGAGAAAGCTTCAGCTATATCGTGTATATG 1734  
QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555  
Db 1735 AAAGACCATCCTGGATCAATAGAGGAAGATGCTCTCAATCATATCAACGCCATGATCAGT 1794  
QY 556 AspAlaIleArgGluLeuAsnTrpGluLeuLysProAspAsnSerValProIleThr 575  
Db 1795 GATGCAATCAGAGAATTAAATTGGGAGCTTCTCAGACCGGATAGCAAAAGTCCCATCTCT 1854  
QY 576 SerLysLysHisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAsp 595  
Db 1855 TCCAAGAAACATGCTTTTGACATCACCAGAGCTTTCCATCATGTCTACAAATATCGAGAT 1914  
QY 596 GlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGluPro 615  
Db 1915 GGTTACACTGTTTCCAACAACGAAACAAAGAATTTGGTGATGAAACCGTCTTCTTGAACCT 1974  
QY 616 ValProLeu 618  
Db 1975 CTCGCTTTG 1983  
RESULT 14  
AAA38938  
ID AAA38938 standard; DNA; 2089 BP.  
XX  
AC AAA38938;  
XX  
DT 25-AUG-2000 (first entry)  
XX  
DE Grand fir limonene synthase DNA sequence SEQ ID NO:57.  
XX  
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;  
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;  
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;  
KW defensive agent; pigment; antitumour; steroid hormone;  
KW signal transduction pathway; bile acid; affinity purification;  
KW photoreceptor; enzymatic synthesis; nutrient supplement;  
KW immunological reagent; ds.  
XX  
OS Abies grandis.  
XX  
PN WO200017327-A2.  
XX  
PD 30-MAR-2000.  
XX  
PF 17-SEP-1999; 99WO-US021419.  
XX  
PR 18-SEP-1998; 98US-0100993P.

PR 22-APR-1999; 99US-0130628P.  
PR 23-AUG-1999; 99US-0150262P.  
XX (KENT ) UNIV KENTUCKY RES DEPT.  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Chappell J, Manna KR, Noel JP, Starks CM;  
XX WPI; 2000-292839/25.  
DR P-PSDB; AAY90859.  
XX  
PT Novel terpene synthase enzymes, useful for producing terpene  
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known  
PT enzymes by specific amino acid alterations.  
XX  
PS Disclosure; Page 445-448; 450pp; English.  
XX  
CC The present invention describes an isolated terpene synthase (I)  
CC comprising a region with at least 20% identity to region 265-535 of a 548  
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha  
CC -carbon atoms (alphaC) that have interatomic distances, between each  
CC other, within tabulated ranges, have a centre point (within a sphere of  
CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered  
CC arrangement of R groups (defining aa side chains), excluding specific  
CC tabulated arrangements (tables given in the specification). (I), and  
CC related enzymes, are used to produce a wide range of terpenoids (e.g.  
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,  
CC flavours, pheromones, defensive agents, pigments, antitumour agents,  
CC components of signal transduction pathways, precursors of steroid  
CC hormones and bile acids, as photoreceptors and as co-factor side chains.  
CC Some synthases with little or no catalytic activity (and nucleic acids  
CC encoding them) are used as controls in the analysis of products formed by  
CC enzymatic synthesis; as nutrient supplements; for affinity purification  
CC of isoprenoids; or to develop immunological reagents or nucleic acids for  
CC monitoring expression of terpene synthase or inheritance of the gene in  
CC plant breeding programs. The new synthases may produce novel terpene  
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.08e-200 Length: 2089  
Score: 2031.50 Matches: 409  
Percent Similarity: 76.67% Conservative: 84  
Best Local Similarity: 63.61% Mismatches: 119  
Query Match: 62.49% Indels: 31  
DB: 3 Gaps: 14  
  
US-10-025-145A-65 (1-618) x AAA38938 (1-2089)  
QY 1 MetAlaLeuLeuSerIleThrProLeu---ValSerArgSerCys----- 14  
Db ATGGCTCTCTTCTATCGTATCTTTGCAGGTTCCCAATCTCTGGGGTGAAATCGTTG 132  
QY 15 LeuSerSerSerHisGluIleLysAlaLeu-----ArgArgThrIleProThrLeuGly 32  
Db ATCAGTTCAGCAATGTGCAGAGGCTCTCTGTATCTCTACAGCAGTCCCAACACTCAGA 192  
QY 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52  
Db ATGCGTAGGCGACAGAAAGCTCTGGTC-----ATCAACATGAAATGACCACGTGTATCC 246  
QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnTyrHisSerAsn 67  
Db CATCGTGATGATAATGGTGGTGGTGTACTGCAAGACGCATAGCCGATCATCCCCAAC 306  
QY 68 LeuTrpAspAspPheIleGlnSerLeuIleSerThrProTyrGlyAlaProAspTyr 87  
Db CTGTGGGAAGATGATTTCATACATCATTTG---TCCTCACCTTATGGGGGATCTTCGTAC 363  
QY 88 ArgGluArgAlaAspArgLeuIleGlyGluValLysAspIleMetPheAsnPhe----- 105  
DB |||||||: : : : : |||||||: : : : : |||||||

Db 364 AGTGAAACGTGCTGACACAGTCGTTGAGGAAGTAAAAAGAG--ATGTTCAATTCAATACCA 420  
QY 106 -----LysSerLeuGluAspGlyGlyAsnAspLeuGlnArgLeuLeuValAsp 123  
Db AATAATAGAGAATATTGTTGCCCAAAATGATCTCCTTACACGCCCTTTGGATGGTGGAT 480  
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThrAlaLeuAsp 143  
Db AGCATTTGAACGCTGGGGATAGATAGACATTTCCAAATGAGATAAGAGTAGCCCTCGAT 540  
QY 144 TyrValAsnSerTyrTrpAsnGluLys---GlyIleGlyCysGlyArgGluSerValVal 162  
Db TATGTTTACAGTTATTGGAAGGAAAGGAGGAGCATTTGGGTGTGGCAGAGATTCTACTTTT 600  
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrVal 182  
Db CCTGATCTCAACTCGACTGCCTTGGCGCTTCGAACCTCTTCGACTGCACGGATACAATGTG 660  
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202  
Db TCTTCAGATGTGCTGGAATACTTCAAGATGAAAAGGGGCATTTTGCTGCCTGCA--- 717  
QY 203 IleGlnIleGluGlyGluIle---ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221  
Db ATCCTTAACCGAGGACAGATCACTAGAACTGTTCTAAATTTATATCGGGCTTCCTGGTC 777  
QY 222 AlaPheProGlyGluLysValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241  
Db GCCTTTCCCGGGAGAAAGTTATGGAAGAGGCTGAAATCTTCTCGGCATCTTATTGAAA 837  
QY 242 GluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspValLeu 261  
Db AAAGTCTTACAAAAGATTCCGGTCTCCAAT---CTTTCAGGAGAGATAGAATATGTTTG 894  
QY 262 GluTyrGlyTyrHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPhe 281  
Db GAATATGTTGGCACACGAATTTGCCGAGATTGGAAGCAAGAAATTATATCGAGGTCTAC 954  
QY 282 -----GlyGlnHisThrLysAsnLysAsnAla-----AlaGluLysLeuLeu 295  
Db GAGCAGAGCGGCTATGAAAGCTTAAACGAGATGCCATATATGAACATGAAGAAGCTTTTA 1014  
QY 296 GluLeuAlaLysLeuGluPheAsnIlePheHisSerLeuGlnGluArgGluLysHis 315  
Db CAACTTGCAAAATTTGGAGTTCAATATCTTTCACCTCTTTGCAACTAAGAGAGTTACAATCT 1074  
QY 316 ValSerArgTrpTrpLysAspSerGlySerProGluMetThrPheCysArgHisArgHis 335  
Db ATCTCCAGATGGTGGAAGAATCAGGTTCTGCTCAACTGACTTTTACACGGCATCGTCAC 1134  
QY 336 ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArg 355  
Db GTGGAATACTACACTATGGCATCTTGCATTTCTATGTTGCCAAAACATTCAGCTTTTCAGA 1194  
QY 356 LeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetTyrAspValPhe 375  
Db ATGGAGTTTGTCAAAGTGTGTCTCTTGTAAACAGTTCTCGATGATATATATGACACTTTT 1254  
QY 376 GlyThrValAspGluLeuGluPheThrAlaThrIleLysArgTrpAspProSerAla 395  
Db GGAACAATGAACGAACCTCCAACCTTTTACGGATGCAATTAAAGAGATGGGATTTGTCAACG 1314  
QY 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn 415  
Db ACAAGGTGCTTCCAGAAATATATGAAAGGAGTGTACATGGACTTGTATCAATGCATTAAT 1374  
QY 416 GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln 435  
Db GAAATGTGGAAGAGGCTGAGAAGACTCAAGGCCGAGATATGCTCAACTATATTCAAAT 1434  
QY 436 AlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyr 455  
Db GCTTGGGAAGCCCTATTTTGATACCTTATGCAAGCAAGCAAGTGGATCTCCAGCAGTTAT 1494



QY 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475  
|||||  
Db 1495 CTCCCAACGTTTGGAGGAGTACTTGAAGAAATGCAAAAGTTAGTCTCGGTCTCGCATAGCC 1554  
  
QY 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495  
|||||  
Db 1555 ACATTACAACCATCTCACTTTGGATGATGACCACTTCTGATTACATACAGTCAAGAAATT 1614  
  
QY 496 AspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515  
|||||  
Db 1615 GATTATCCATCCAGATTCAATGAGTTAGTTGCTCGTCCATCCTTCGACTACGAGGTGACACG 1674  
  
QY 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535  
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Db 1675 CGCTGCTACAGCGGATAGGCCCCGTGGAGAAGAAGCTTCAGCTATATCGTGTATATG 1734  
  
QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555  
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Db 1735 AAAGACCATCTCGATCAATAGAGGAAGATGCTCTCAATCATATCAACGCCATGATCAGT 1794  
  
QY 556 AspAlaIleArgGluLeuAsnTrpGluLeuLysProAspAsnSerValProIleThr 575  
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Db 1795 GATGCAATCAGAGAATTAAATTGGGAGCTTCTCAGACCGGATAGCAAAAGTCCCATCTCT 1854  
  
QY 576 SerLysLysHisAlaPheAspIleSerArgValTrpHisGlyTyrArgTyrArgAsp 595  
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Db 1855 TCCAAGAAACATGCTTTTGACATCACAGAGCTTCCATCATGTCTACAAATATCGAGAT 1914  
  
QY 596 GlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGluPro 615  
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Db 1915 GGTTACACTGTTTCCAACAACGAAACAAAGAATTGGTGATGAAACCGTTCTTGAACCT 1974  
  
QY 616 ValProLeu 618  
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Db 1975 CTCGCTTTG 1983

RESULT 15

AAAF73373  
ID AAF73373 standard; cDNA; 2089 BP.

XX AAF73373;

DT 30-APR-2001 (first entry)

DE Grand fir (-)-limonene synthase coding sequence SEQ ID NO: 5.

XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;  
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;  
KW terpinolene synthase; insect resistance; nutrition; ss.

XX Abies grandis.

XX WO200107565-A2.

XX 01-FEB-2001.

PF 24-JUL-2000; 2000WO-US020264.

XX 26-JUL-1999; 99US-00360545.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Steele CL, Bohlmann J, Croteu RB, Phillips MA;

DR WPI; 2001-182782/18.

XX P-PSDB; AAB69372.

XX New nucleic acid encoding monoterpene synthases, for increasing terpene  
PT synthesis in plants, e.g. for increasing resistance to pests or for  
PT treatment of cancer.

XX Claim 33; Page 112-115; 175pp; English.

XX

CC The present invention provides the protein and coding sequences of  
CC monoterpene synthases from the grand fir. These include (-)-camphene  
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-  
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase  
CC and pinene synthase. The sequences can be used to produce transgenic  
CC plants expressing high levels of the enzymes, resulting in levels which  
CC are useful in protecting against and treating cancers, and to confer  
CC insect resistance on plants

XX Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.08e-200 Length: 2089  
Score: 2031.50 Matches: 409  
Percent Similarity: 76.67% Conservative: 84  
Best Local Similarity: 63.61% Mismatches: 119  
Query Match: 62.49% Indels: 31  
DB: 4 Gaps: 14

US-10-025-145A-65 (1-618) x AAF73373 (1-2089)

QY 1 MetAlaLeuLeuSerIleThrProLeu--ValSerArgSerCys----- 14  
Db 73 ATGGCTCTCTTCTATCGTATCTTTCGAGGTTCCCAATCCTGCGGGTGAAATCGTTG 132  
  
QY 15 LeuSerSerHisGluIleLysAlaLeu-----ArgArgThrIleProThrLeuGly 32  
::: |||||  
Db 133 ATCAGTTCAGCAATGTGCAGAAGGCTCTGTATCTCTACAGCAGTCCCAACTCAGA 192  
  
QY 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52  
::: |||||  
Db 193 ATGCGTAGCGACAGAAAGCTCTGGTC-----ATCAACATGAAATTGACCACTGTATCC 246  
  
QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnTyrHisSerAsn 67  
||| |||||  
Db 247 CATCGTGATGATAATGGTGGTGTGTTACTGCAAGACGCATAGCCGATCATCCCAAC 306  
  
QY 68 LeuTrpAspAspPheIleGlnSerLeuIleSerThrProTyrGlyAlaProAspTyr 87  
|||||  
Db 307 CTGTGGGAAGATGATTTCATACAATCATTTG---TCCTCACCTTATGGGGATCTTCGTAC 363  
  
QY 88 ArgGluArgAlaAspArgLeuIleGlyGluValLysAspIleMetPheAsnPhe----- 105  
|||||  
Db 364 AGTGAACGTGCTGAGACAGTCGTTGAGGAAGTAAAGAG---ATGTTCAATTCAATACCA 420  
  
QY 106 -----LysSerLeuGluAspGlyGlyAsnAspLeuGlnArgLeuLeuValAsp 123  
::: |||  
Db 421 AATAATAGAGAATTATTTGGTTCCCAAAATGATCTCTTACACGCCCTTTGGATGGAT 480  
  
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThrAlaLeuAsp 143  
::: |||||  
Db 481 AGCATTGAACGCTGTGGGATAGATAGACATTCCAAAATGAGATAAGTAGCCCTCGAT 540  
  
QY 144 TyrValAsnSerTyrTrpAsnGluLys---GlyIleGlyCysGlyArgGluSerValVal 162  
|||||  
Db 541 TATGTTTACAGTTATTGGAAGGAAAGGAGGCATTTGGTGTGGCAGAGATTCTACTTTT 600  
  
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrVal 182  
|||||  
Db 601 CCTGATCTCAACTCGACTGCCTTGGCGCTTCGAACTCTTCGACTGCACGAGATACAATGTG 660  
  
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202  
|||||  
Db 661 TCTTCAGATGTGCTGGAATACTTCAAAGATGAAAAGGGGCATTTTGCCTGCCCTGCA--- 717  
  
QY 203 IleGlnIleGluGlyGluIle---ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221  
||| |||||  
Db 718 ATCTTAACCGAGGACAGATCACTAGAACTGTTCTAAATTTATATCGGGCTTCCTGGTC 777  
  
QY 222 AlaPheProGlyGluLysValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241  
|||||  
Db 778 GCCTTTCCCGGAGAGAAAGTTATGGAAGAGGCTGAAATCTTCTCGGCATCTTATTGAAA 837



QY	242	GluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspValLeu	261
Db	838	AAAAGTCTTACAAAAGATTCCGGTCTCCAAT---CTTTCAGGAGAGATAGAAATATGTTTTG	894
QY	262	GluTyrGlyTrpHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPhe	281
Db	895	GAATATGTTGGCACACGAATTTGCCGAGATTGGAAGCAAGAAATATATCGAGGTCTAC	954
QY	282	-----GlyGlnHisThrLysAsnLysAsnAla-----AlaGluLysLeuLeu	295
Db	955	GAGCAGAGCGGCTATGAAAGCTTAAACGAGATGCCATATATGAACATGAAGAAGCTTTTA	1014
QY	296	GluLeuAlaLysLeuGluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHis	315
Db	1015	CAACTTGCAAAATTGGAGTTCAATATCTTTCACTCTTTGCAACTAAGAGAGTTACAATCT	1074
QY	316	ValSerArgTrpTrpLysAspSerGlySerProGluMetThrPheCysArgHisArgHis	335
Db	1075	ATCTCCAGATGGTGGAAAGAATCAGGTTTCGTCTCAACTGACTTTTACACGGCATCGTCAC	1134
QY	336	ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArg	355
Db	1135	GTGGAATACTACACTATGGCATCTTGCAATTTCTATGTGCCAAACATTCAGTTTCAGA	1194
QY	356	LeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetIleArgValPhe	375
Db	1195	ATGGAGTTTGTCAAAGTGTGTCTATCTTGTAACAGTCTCGATGATATATGACACTTTT	1254
QY	376	GlyThrValAspGluLeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAla	395
Db	1255	GGAACAAATGAACGAACCTCCAACCTTTTACGGATGCCAATTAAAGAGATGGGATTTGTCAACG	1314
QY	396	MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn	415
Db	1315	ACAAGGTGGCTTCCAGAATATATGAAAGGAGTGTACATGGACTTGTATCAATGCATTAAT	1374
QY	416	GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln	435
Db	1375	GAAATGGTGGAGAGGCTGAGAAGACTCAAGGCCGAGATATGCTCAACTATATTCAAAAT	1434
QY	436	AlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyr	455
Db	1435	GCTTGGGAAGCCCTATTGTATACCTTTATGCAAGCAAGTGGATCTCCAGCAGTTAT	1494
QY	456	LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys	475
Db	1495	CTCCCAACGTTTGAGGAGTACTTGAAGAATGCAAAAGTTAGTTCTGGTTCTGCATAGCC	1554
QY	476	AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal	495
Db	1555	ACATTACAACCCATTCTCACTTTGGATGTACCACCTTCCTGATTACATACTGCAAGAAAT	1614
QY	496	AspPheProSerLysLeuAsnAspLeuIleCysIleLeuArgLeuArgGlyAspThr	515
Db	1615	GATTATCCATCCAGATTCAATGAGTTAGTTTCGTTCATCTTCGACTACGAGGTGACACG	1674
QY	516	ArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet	535
Db	1675	CGCTGCTACAAGCGGATAGGGCCCGTGGAGAAGAAGCTTCAGCTATATCGTGTATATG	1734
QY	536	LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg	555
Db	1735	AAAGACCATCCTGGATCAATAGAGGAAGATGCTCTCAATCATATCAACGCCCATGATCAGT	1794
QY	556	AspAlaIleArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThr	575
Db	1795	GATGCAATCAGAGAAATTAATTGGGAGCTTCTCAGACCGGATAGCAAAAGTCCCATCTCT	1854
QY	576	SerLysLysHisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAsp	595
Db	1855	TCCAAGAAACATGCTTTTGACATCACCAGAGGTTTCCATCATGCTTACAAATATCGAGAT	1914

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 8, 2004, 15:05:55 ; Search time 4324 Seconds  
(without alignments)  
4267.999 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
Sequence: 1 MALLSITPLVSRSLSSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10025145/runat\_07072004\_160150\_27949/app\_query.fasta\_1.775  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10025145@cgn\_1\_1\_3437@runat\_07072004\_160150\_27949 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mus:\*  
23: em\_gss\_pro:\*  
24: em\_gss\_rod:\*  
25: em\_gss\_phg:\*  
26: em\_gss\_vrl:\*  
27: em\_gss1:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1066	32.8	745	14	CF477103	CF477103 RTWW3_5_A
2	907	27.9	700	14	CF474786	CF474786 RTWW2_7_B
3	888	27.3	696	14	CF401916	CF401916 RTWW1_15
C 4	872	26.8	669	14	CF479802	CF479802 RTWW3_12
5	864	26.6	697	13	BQ196773	BQ196773 NXLV105_B
6	853	26.2	599	13	BX680641	BX680641 EX680641
7	802	24.7	599	12	BG526917	BG526917 NXPV_057
8	795	24.5	804	14	CF666338	CF666338 RTCNT1_22
9	786	24.2	616	14	CF6663845	CF6663845 RTCNT1_5
10	764	23.5	637	14	CF476978	CF476978 RTWW3_5_A
11	733	22.5	481	9	AL750951	AL750951 AL750951
C 12	723	22.2	740	14	CF477562	CF477562 RTWW3_8_G
13	717	22.1	516	13	BQ698077	BQ698077 NXPV_064
14	713	21.9	517	13	BX677624	BX677624 BX677624
15	698	21.5	539	10	AW287756	AW287756 EST0004_S
16	681	20.9	569	10	AW287754	AW287754 EST0002_S
17	680	20.9	557	14	CF666483	CF666483 RTCNT1_23
C 18	658	20.2	651	14	CF479884	CF479884 RTWW3_12
19	657.5	20.2	534	10	AW287755	AW287755 EST0003_S
20	656	20.2	682	14	CF663768	CF663768 RTCNT1_5
21	607	18.7	430	13	BQ702557	BQ702557 NXSI_129
22	587.5	18.1	591	14	CA305371	CA305371 hasp004xk
23	579.5	17.8	2029	11	AY107369	AY107369 Zea mays
24	559	17.2	618	9	AL750955	AL750955 AL750955
25	550	16.9	541	14	CF672979	CF672979 RTCNT1_75
26	526.5	16.2	725	14	CF397293	CF397293 RTDS3_2_A
27	525	16.1	542	10	BG039521	BG039521 NXSI_099
28	517.5	15.9	1981	11	AY105371	AY105371 Zea mays
29	515.5	15.9	725	14	CF470471	CF470471 RTDS1_17
30	507.5	15.6	629	9	AU299287	AU299287 AU299287
31	496.5	15.3	843	14	CF208265	CF208265 CAB20003
32	489	15.0	574	14	CF474640	CF474640 RTWW2_7_B
33	489	15.0	733	14	CF666270	CF666270 RTCNT1_22
34	488	15.0	2028	11	AY110842	AY110842 Zea mays
35	481	14.8	730	13	BX682869	BX682869 BX682869
36	477.5	14.7	896	29	CG847800	CG847800 ZMMBB031
37	476	14.6	634	14	CF397946	CF397946 RTDS3_23
38	475	14.6	597	14	CF666416	CF666416 RTCNT1_23
39	465.5	14.3	585	12	BG318038	BG318038 NXPV_008
40	453	13.9	574	9	AW065088	AW065088 ST39E04_P
41	446.5	13.7	766	13	BU814724	BU814724 N032C12_P
42	439.5	13.5	552	13	BQ696096	BQ696096 NXPV_036
C 43	429.5	13.2	530	9	AU298829	AU298829 AU298829
44	427	13.1	760	12	BG351484	BG351484 l11F08_Ma
45	418.5	12.9	824	14	CD852160	CD852160 DH0ALL25Z

ALIGNMENTS

RESULT 1  
CF477103  
LOCUS  
DEFINITION  
CF477103 745 bp mRNA linear EST 08-SEP-2003  
RTWW3\_5\_A06.g1\_A022 Well-watered loblolly pine roots WW3 Pinus  
taeda cDNA clone RTWW3\_5\_A06\_A022 5', mRNA sequence.  
ACCESSION  
CF477103  
VERSION  
CF477103.1 GI:34505972  
KEYWORDS  
EST.  
SOURCE  
Pinus taeda (loblolly pine)  
ORGANISM  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus;  
REFERENCE  
1 (bases 1 to 745)

AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.

TITLE An EST database from well-watered loblolly pine (Pinus taeda) roots

JOURNAL Unpublished (2003)

COMMENT Other\_ESTs: RTWW3\_5 A06.b1\_A022

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAAACAGCTATGACC).

Location/Qualifiers

1..745

/organism="Pinus taeda"

/mol\_type="mRNA"

/strain="CCLONES"

/db\_xref="taxon:3352"

/clone="RTWW3\_5 A06\_A022"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Well-watered loblolly pine roots WW3"

/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:

Pred. No.: 4.36e-112 Length: 745

Score: 1066.00 Matches: 195

Percent Similarity: 87.90% Conservative: 23

Best Local Similarity: 78.63% Mismatches: 30

Query Match: 32.79% Indels: 0

DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF477103 (1-745)

QY 356 LeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspMetTyrAspValPhe 375

Db 2 CTCGGCTTGGCAAATCCTGTCTATCATCATCACCGTTCTGTATGATGATGACGACCTTC 61

QY 376 GlyThrValAspGluLeuGluPheThrAlaThrIleLysArgTrpAspProSerAla 395

Db 62 GGAACACTCGACGAGCTCGAACTCTTCACAGCTGCAATTAAAGAGATGGATCCGTCGGCG 121

QY 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn 415

Db 122 ACAGAGTGCCTTCCAGAAATATATGAAAGGAGTTTACATGATAGTTTACAACACTGTAAAT 181

QY 416 GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln 435

Db 182 GAAATGCTCAGGAGGCGACAGACAGGCTCAAGGCCGAGACACGCTCAACTATTGTGCGACAG 241

QY 436 AlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyr 455

Db 242 GCTTGGAGGAATATATTGATTCGTATATGCAAGCAAGCAAGTGGATCGCCAGTGGTGAG 301

QY 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475

Db 302 GTGCCAACATTTGAGGAGTACTACGAGAACGGGAAATTAGCTCTGGTCTATCGCGTATCG 361

QY 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495

Db 362 GCATTGCAACCCATTCTGACGACCGACATCCCTTTCCTGAGCAGCTCCTCAAGGAAGCT 421

QY 496 AspPheProSerLysLeuAsnAspLeuIleCysIlelleLeuArgLeuArgGlyAspThr 515

Db 422 GACATTCCATCGAAGCTCAATGACTTGGCATCTGCCATTCTTCGATTACGAGGAGATACG 481

QY 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535

Db 482 CGCTGCTACAGCGGACAGGGCCCGTGGAGAAGACTTCGTGTATATCTTGTATATG 541

QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555

Db 542 AAAGACAAATCCTGGAGCAACGGGAAGAGATGCTCTCAATCATATCAACGCCATGATCAGT 601

QY 556 AspAlaIleArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThr 575

Db 602 GATGTAATTAAAGGATTAAATTGGAGCTTCTCAAACCAACAGCAGCGTCCCATATCT 661

QY 576 SerLysLysHisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAsp 595

Db 662 GCCAAAAACATGCTTTTGACATTAGCAGAGCTTTCATTATGGCTACAAATATCGAGAT 721

QY 596 GlyTyrSerPheAlaAsnValGlu 603

Db 722 GGCTACAGCGTTGCCAGCATTGAA 745

RESULT 2

CF474786 700 bp mRNA linear EST 05-SEP-2003

LOCUS RTWW2\_7\_B11.g1\_A021 Well-watered loblolly pine roots WW2 Pinus

DEFINITION taeda\_cDNA clone RTWW2\_7\_B11\_A021 5', mRNA sequence.

ACCESSION CF474786

VERSION CF474786.1 GI:34492158

KEYWORDS EST.

SOURCE Pinus taeda (loblolly pine)

ORGANISM Pinus taeda

REFERENCE 1 (bases 1 to 700)

AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.

TITLE An EST database from well-watered loblolly pine (Pinus taeda) roots

JOURNAL Unpublished (2003)

COMMENT Other\_ESTs: RTWW2\_7\_B11.b1\_A021

Contact: Cordonnier-Pratt MM

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Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAAACAGCTATGACC).

Location/Qualifiers

1..700

/organism="Pinus taeda"

/mol\_type="mRNA"

/strain="CCLONES"

/db\_xref="taxon:3352"

/clone="RTWW2\_7\_B11\_A021"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Well-watered loblolly pine roots WW2"

/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine



(Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:  
Pred. No.: 9.79e-94 Length: 700  
Score: 907.00 Matches: 160  
Percent Similarity: 84.98% Conservative: 38  
Best Local Similarity: 68.67% Mismatches: 35  
Query Match: 27.90% Indels: 0  
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF474786 (1-700)

QY 334 ArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGly 353  
Db 2 CGTCAGTGGAACTACTACACTTTAGCAGCTTGCAATGCAATGATCCTAAACATTCTGCG 61  
QY 354 PheArgLeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspMetTyrAsp 373  
Db 62 TTTCGACTAGGATTGGTAAATAAGTCATATGATCAGGATTCGACGATATCTACGAC 121  
QY 374 ValPheGlyThrValAspGluLeuGluLeuPheThrAlaThrIleLysArgTrpAspPro 393  
Db 122 ACCTTCGGAACAATGGAGGAGCTCGAACTCTTAACCGCAGCGTTTAAGAGATGGATCCG 181  
QY 394 SerAlaMetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThr 413  
Db 182 TCTTCGATAGAGTGCTTCCAGATTATATGAAGGAGGTGTACATGGCGGTTTACGACAAC 241  
QY 414 ValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAla 433  
Db 242 ATCAACGAATGGCAGGAGGGCGAGAAATTCAGGCTGGGATACAGTCACTATGCT 301  
QY 434 ArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThr 453  
Db 302 CGAAATCTTCGGAGGCTTTATTGGTGCTTATATACAGAAGCCAACTGGATTCCAGT 361  
QY 454 GlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArg 473  
Db 362 GGTTATCTTCCACGTTTCGACGAGTACCTCGAGAATGGGAAGGTCACTCGGCTCTCGC 421  
QY 474 ProCysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLys 493  
Db 422 ATAACCACGCTCGAACCCATGCTGACTTTGGGGTTTCTCTTCGCGCTCGAATCCTGCAG 481  
QY 494 GluValAspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGly 513  
Db 482 GAAATTGACTTCCATCGAAATTCATGATTGTATATGTGCCATCTTCGACTGAAAGGT 541  
QY 514 AspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCys 533  
Db 542 GACACTCAATGCTACAAGGCTGACAGGCGCGTGGAGAAGAGCTTCGGCGGTATCGTGT 601  
QY 534 TyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMet 553  
Db 602 TATATGAAGACCATCTCTGGAATAACAGAGGAAGATGCTGTCAATCAAGTCAATGCTATG 661  
QY 554 IleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeu 566  
Db 662 GTCGATAACTTAACCAAGGAAGTGAATGGGAGTTACTT 700

RESULT 3

CF401916 696 bp mRNA linear EST 29-AUG-2003  
LOCUS RTW1\_15\_B05.g1\_A015 Well-watered loblolly pine roots WW1 Pinus  
DEFINITION taeda cDNA clone RTW1\_15\_B05\_A015 5', mRNA sequence.  
ACCESSION CF401916  
VERSION CF401916.1 GI:34360333  
KEYWORDS EST.

SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
REFERENCE 1 (bases 1 to 696)  
AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.

TITLE An EST database from well-watered loblolly pine (Pinus taeda) roots  
JOURNAL Unpublished (2003)  
COMMENT Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAAACAGCTATGACC).

FEATURES  
source

Location/Qualifiers  
1..696  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTW1\_15\_B05\_A015"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WW1"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:  
Pred. No.: 1.53e-91 Length: 696  
Score: 888.00 Matches: 156  
Percent Similarity: 84.48% Conservative: 40  
Best Local Similarity: 67.24% Mismatches: 36  
Query Match: 27.31% Indels: 0  
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF401916 (1-696)

QY 344 CysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHis 363  
Db 1 TGCATTGCAATGATCCTAAACATTTTGGCTTCGACTAGGATTTGGTAAATAAGTCAT 60  
QY 364 LeuIleThrValLeuAspMetTyrAspValPheGlyThrValAspGluLeuGluLeu 383  
Db 61 ATGATCAGGATTCGACGATATCTACGACACCTTCGGAACAATGGAGGAGCTCGAATC 120  
QY 384 PheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMet 403  
Db 121 TTAACCGCAGCGTTTAAGAGATGGGATCCGTTCTTCGATAGAGTGTCTCCAGATTATATG 180  
QY 404 LysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLys 423  
Db 181 AAAGGAGTGATACATGGCGGTTTACGACAACATCAACGAAATGGCAGAGGCGCAGAAA 240  
QY 424 AlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSer 443  
Db 241 ATCAAGGCTGGGATACAGTCAGCTATGCTCGAAAAATCTTGGGAGGCTTTTATTGTGCT 300



ACCESSION BQ196773  
VERSION BQ196773.1 GI:20379276  
KEYWORDS EST.  
SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. Sederoff,R.  
REFERENCE 1 (bases 1 to 697)  
AUTHORS Molecular Basis of Wood Formation in the Pine Megagenome  
TITLE Unpublished (2000)  
JOURNAL  
COMMENT Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh, NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron\_sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further information.  
Seq primer: T3.

FEATURES  
source  
1. .697  
/location/Qualifiers  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NX1V105 B02"  
/tissue\_type="primary xylem"  
/dev\_stage="late wood"  
/lab\_host="XL1-Blue"  
/clone\_lib="NX1V (Nsf Xylem Late wood Vertical)"  
/note="Vector: pTriplex; Site 1: EcoRI; The library is from late (summer-August) wood, taken from below the crown of a 20 year old tree. The harvested xylem tissue was on the cusp between transitional and mature wood. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCCATTATGGCC'."

ORIGIN

Alignment Scores:  
Pred. No.: 9.21e-89 Length: 697  
Score: 864.00 Matches: 162  
Percent Similarity: 85.45% Conservative: 20  
Best Local Similarity: 76.06% Mismatches: 31  
Query Match: 26.58% Indels: 0  
DB: 13 Gaps: 0

US-10-025-145A-65 (1-618) x BQ196773 (1-697)

QY 406 ValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGln 425  
Db 23 GTTTACATGATAGTTTACAACACTGTAAATGAAATGTCTCAGGAGGCACACAAGGCTCAA 82  
QY 426 GlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMet 445  
Db 83 GGCCGAGACACGCTCAACTATTGTCGACAGCGCTGGGAGGAATATATTGATCGGTATATG 142  
QY 446 GlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsn 465  
Db 143 CAAGAAGCAAAGTGGATCGCCCGTGGTGAGTGCCCAACATTTGAGGAGTACTATGAGAAC 202  
QY 466 GlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIle 485  
Db 203 GGGAAAGTTAGTCTGGTCATCGCGTATCGGCATTGCAACCCATTCTGACGCCGACATC 262  
QY 486 PropheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIle 505  
Db 263 CCCTTTCTGAGCAGCGTCCTCAAGGAAGTTGACATTCATCGAAGCTCAATGACTTGGCA 322  
QY 506 CysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGly 525

Db 323 TCTGCCATTCTTCGATTACGAGGGGATACGGCTGTACAGGGGACAGGCCCGTGA 382  
QY 526 GluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAsp 545  
Db 383 GAAGAAGCTTCGTGTATATCTTGTATATGAAAGACAATCCTGGAACAACAGAGGAAGAT 442  
QY 546 AlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeu 565  
Db 443 GCTCTCAATCATCTCAACGCCCATGATCAGTGTATTAATAAGGATTAAATTGGAGCTT 502  
QY 566 LeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArg 585  
Db 503 CTCAAAATCAAACAGCAGCGTTCCCATATCTGCCAAAAAACATGCTTTTGACATTAGCAGA 562  
QY 586 ValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLys 605  
Db 563 GCTTTCATTGTGGCTACAAATATCGAGATGGCTACAGCGTTGCCAACATTGAAACNNNN 622  
QY 606 SerLeuValMetArgThrValIleGluProValProLeu 618  
Db 623 NGTTTGGTGANNNNNACCGTCATTGATCCTGTCACCTTTA 661

RESULT 6

BX680641

LOCUS

DEFINITION BX680641 RS Pinus pinaster cDNA clone RS46D06, mRNA

ACCESSION BX680641

VERSION BX680641.1 GI:38015099

KEYWORDS EST.

SOURCE Pinus pinaster

ORGANISM Pinus pinaster

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 599)

AUTHORS Frigerio, J. and Plomion, C.

TITLE Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach

JOURNAL Unpublished (2002)

COMMENT Contact: Frigerio JM

Genetique et Amelioration 69

INRA

route d'Arcachon 33612 Cestas CEDEX France

Email: Frigerio@pierroton.inra.fr

Email: Frigerio@pierroton.inra.fr

Seq primer: T3.

Location/Qualifiers

1. .599

/organism="Pinus pinaster"

/mol\_type="mRNA"

/db\_xref="taxon:71647"

/clone="RS46D06"

/tissue\_type="root"

/dev\_stage="6 weeks old seedling"

/lab\_host="SOLR"

/clone\_lib="RS"

/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN

Alignment Scores:

Pred. No.: 1.31e-87 Length: 599

Score: 853.00 Matches: 161

Percent Similarity: 87.94% Conservative: 14

Best Local Similarity: 80.90% Mismatches: 24

Query Match: 26.24% Indels: 1



DB: 13 Gaps: 0

US-10-025-145A-65 (1-618) x BX680641 (1-599)

Qy	399	LeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAla	418
Db	3	CTTCCACATATATGAAAGGAAT-TACATGATGGTTTACAACACCGTAAATGAAATGTCT	61
Qy	419	ArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGlu	438
Db	62	GCGGAGGCACAGAGGCTCAAGGCCGAGACACTCTCAACTATGCTCGACAGGCTTGGGAG	121
Qy	439	AlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThr	458
Db	122	GATTATCTTGATTCGTATATGCAAGAACAAAGTGGATAGCCACGGGTATCTGCCAACG	181
Qy	459	pheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGln	478
Db	182	TTTCGAGGAATACTTGGAGAACGGGAAAGTTAGCTCTGGCATCGCGTCTGGCGTTGCAA	241
Qy	479	ProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPhePro	498
Db	242	CCCATGCTGACGATGGACATCCCCCTTCCCTCCTCACATCCTCAAGGAAGTTGACTTCCCA	301
Qy	499	SerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyr	518
Db	302	TCCAACCTCAATGACTTGGCATGTGCCATACTTCGATTACGAGGTGATACCCGATGTTAT	361
Qy	519	LysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsn	538
Db	362	CAGGAGGACAGGCTCGTGGAGAGAAACCTCGTGTATATCTTGTATTATGAAAGACAAC	421
Qy	539	ProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIle	558
Db	422	CCTGGAGCAACAGAGGAAGATGCTCTTAATCATCTCAATGTATCATGATCAGTGGCGTAATT	481
Qy	559	ArgGluLeuAsnTrpGluLeuLysProAspAsnSerValProIleThrSerLysLys	578
Db	482	AAAGAATTAATTTGGGAGCTTCTCAAACCCGACAACAGTGTGCCCATTTCTTCCAAAGAAA	541
Qy	579	HisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyr	597
Db	542	ATTACTTTTGACATTAACAGAGCTTTCCATTACGGTTACAATACCGAGATGGCTAC	598

RESULT 7

BG526917

LOCUS

DEFINITION

BG526917 599 bp mRNA linear EST 07-MAY-2003

NXPV\_057\_D04\_F\_NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda

CDNA\_clone NXPV\_057\_D04\_5' similar to Arabidopsis thaliana sequence

At4g16730 limonene cyclase like protein see

<http://mips.gsf.de/proj/thal/db/index.html>, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BG526917.1 GI:13536796

pinus taeda (loblolly pine)

Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 599)

Sederoff,R.

Molecular Basis of Wood Formation in the Pine Megagenome

Unpublished (2000)

Contact: Sederoff, Ron

Forest Biotechnology

North Carolina State University

840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh, NC 27695, USA

Tel: 919 515 7800

Fax: 919 515 7801

Email: [ron.sederoff@ncsu.edu](mailto:ron.sederoff@ncsu.edu), [jerri.johnson@ncsu.edu](mailto:jerri.johnson@ncsu.edu)

Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further information.

Seq primer: T3.





The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: JENREV (CAGGAACACGCTATGACC).

FEATURES  
source

Location/Qualifiers  
1..616  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="3 CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTCNT1 5 B08 A029"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Root control"  
/note="Organ: root; Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA cuttings that were rooted and then planted in washed sand. Just before harvesting roots for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:  
Pred. No.: 7.81e-80 Length: 616  
Score: 786.00 Matches: 143  
Percent Similarity: 83.08% Conservative: 24  
Best Local Similarity: 71.14% Mismatches: 34  
Query Match: 24.18% Indels: 0  
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF663845 (1-616)

QY 286 LysAsnLysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePhe 305  
|||  
DB 12 AAGACGACGACCAAGACCGAGAAGCTTTTAGAACTTGCAAAATGGAGTTCAATATCTTT 71  
QY 306 HisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySer 325  
|||  
DB 72 CACTCCTTACAGCAAAAGAGTTAAACAGCTGTCCAGATGGTGGAAGATTCGGGTTTC 131  
QY 326 ProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIle 345  
|||  
DB 132 TCTCAACTGACATTCACCTCGGCATCGTCACGTGGAATTTACACTTTGGCCTCCTGCATT 191  
QY 346 AlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIle 365  
|||  
DB 192 GCCACTGAGCCCAACATTACGATTCAGATTTGGGCTTTGCCAAACGTTATCTTGA 251  
QY 366 ThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThr 385  
|||  
DB 252 ATAGTTCTGGACGACATCTATGACACTTTCGGAACAATGGAGAGCTCGAACTCTTCACA 311  
QY 386 AlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGly 405  
|||  
DB 312 GCCGCAATTAAGAGATGGGATCCCTCCGCGAGGAGTTCTTCAGAAATATATGAAAGGC 371

QY 406 ValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGln 425  
:::|||||::: ||| |||||::: |||||::: |||||::: |||||::: |||||  
DB 372 ATATATATGGTGTGTTTACGATTGCGTTAATCAAATGGCTCGAGAGCGGAGAGTCAA 431  
QY 426 GlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMet 445  
|||  
DB 432 GGCCGAGACACGCTCACCTACGCTCGAAATACGTGGGAAGCCGTTATTTGATGCGTTCTG 491  
QY 446 GlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluTyrLeuGluAsn 465  
:::|||||::: |||||::: |||||::: |||||::: |||||::: |||||  
DB 492 GAAGAAGCAAAAGTGGATGCCAGCGTTATATATACCCACGTTTGAGGAGTATTGGAGAAC 551  
QY 466 GlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIle 485  
|||  
DB 552 GGGAAGGTGAGTTTGGGTATCGAGCAGCCACACTGCAACCCATTCTCAGTTGGATATT 611  
QY 486 Pro 486  
|||  
DB 612 CCC 614

RESULT 10  
CF476978

LOCUS  
DEFINITION  
CF476978 637 bp mRNA linear EST 08-SEP-2003  
taeda cDNA clone RTW3\_5\_A06\_A022 3', mRNA sequence.

ACCESSION  
VERSION

CF476978.1 GI:34505847

KEYWORDS  
SOURCE

pinus taeda (loblolly pine)

ORGANISM  
REFERENCE

Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; 1 (bases 1 to 637)  
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.

TITLE  
JOURNAL

An EST database from well-watered loblolly pine (Pinus taeda) roots Unpublished (2003)

COMMENT

Other\_ESTs: RTW3\_5\_A06.g1\_A022  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: M13-21 (TGTAACACGACGGCCAGT)  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1..637  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="CCLONES"  
/db\_xref="taxon:3352"  
/clone="RTW3\_5\_A06\_A022"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WW3"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/- 0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:
Pred. No.: 2.92e-77 Length: 637
Score: 764.00 Matches: 142
Percent Similarity: 86.41% Conservative: 17
Best Local Similarity: 77.17% Mismatches: 25
Query Match: 23.50% Indels: 0
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF476978 (1-637)
QY 435 GlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGly 454
Db 3 CAGGCTTGGAGGATATATTGATTGTTATATGCAAGAAGCAAAAGTGGATCGCCAGTGT 62
QY 455 TyrLeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgPro 474
Db 63 GAGGTGCCAACATTGAGGAGTACTACGAGAACGGGAAAATTAGCTCTGGTCATCGCGTA 122
QY 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGlu 494
Db 123 TCGGCATTGCAACCCATTCTGACGACCGACATCCCTTTCCTGAGCACGTCCTCAAGGAA 182
QY 495 ValAspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAsp 514
Db 183 GCTGACATTCCATCGAAGCTCAATGACTTGGCATCTGCCATTCTTCGATTACGAGGAT 242
QY 515 ThrArgCysTyrLysAlaAspArgAlaArgGlyGluAlaSerSerIleSerCysTyr 534
Db 243 ACGCGCTGCTACGAGCGGACAGGGCCCGTGGAGAAGAAGCTTCGTGTATATCTTGTAT 302
QY 535 MetLysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIle 554
Db 303 ATGAAAGACAATCCTGGAGCAACGGAAGATGCTCTCAATCATATCAACGCCATGATC 362
QY 555 ArgAspAlaIleArgGluLeuAsnTrpGluLeuLysProAspAsnSerValProIle 574
Db 363 AGTGATGTAATTAAGGATTAAATTGGGAGCTTCTCAAACCAACAGCAGCGTTCCCAT 422
QY 575 ThrSerLysLysHisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArg 594
Db 423 TCTGCCAAAAACATGCTTTTGACATTAGCAGAGCTTTCATTATGGCTACAAATATCGA 482
QY 595 AspGlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGlu 614
Db 483 GATGGCTACAGCGTTGCCAGCATTGAAACAAAGAGTTTGGTGAAGCAACCGTCATTGAT 542
QY 615 ProValProLeu 618
Db 543 GCTGIGACTTTA 554

RESULT 11
AL750951
LOCUS
DEFINITION
AL750951 RS pinus pinaster cDNA clone RS02D01 similar to PINENE SYNTHASE, mRNA sequence.
ACCESSION
AL750951
VERSION
AL750951.1 GI:21492198
KEYWORDS
EST.
SOURCE
Pinus pinaster
ORGANISM
Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 481)
Frigerio,J. and Plomion,C.
Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach
Unpublished (2002)
Contact: Frigerio JM
Genetique et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..481
/organism="Pinus pinaster"
/mol\_type="mRNA"
/db\_xref="taxon:71647"
/clone="RS02D01"
/tissue\_type="root"
/dev\_stage="6 weeks old seedling"
/lab\_host="SOLR"
/clone\_lib="RS"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN
Alignment Scores:
Pred. No.: 6.76e-74 Length: 481
Score: 733.00 Matches: 134
Percent Similarity: 90.62% Conservative: 11
Best Local Similarity: 83.75% Mismatches: 15
Query Match: 22.55% Indels: 0
DB: 9 Gaps: 0

US-10-025-145A-65 (1-618) x AL750951 (1-481)
QY 335 HisValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPhe 354
Db 2 CACGTGGAGTACTACACTTTGGCTTCTCGATCGGTTTGAGCCCCAACATTCTGGATT 61
QY 355 ArgLeuGlyPheThrLysMetSerHisLeulleThrValLeuAspAspMetTyrAspVal 374
Db 62 AGACTCGGCTTTCGAAAGCGTGTCTATATATCACTGTTCTCGACGATATGTACGACCTC 121
QY 375 PheGlyThrValAspGluLeuGluPheThrAlaThrIleLysArgTrpAspProSer 394
Db 122 TTCGAACAGTTGATGAGCTCAAACTGTTACAGCCGCAATTAGAGATGGGATCCGTCC 181
QY 395 AlaMetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrVal 414
Db 182 GCCACAGATTGCCTTCCACAATATATGAAAGGAATTTACATGATGTTTACAACACCGTA 241
QY 415 AsnGluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArg 434
Db 242 AATGAAATGCTCGGAGGCACAGAGGCTCAAGCCGAGACACTCTCAACTATGCTCGA 301
QY 435 GlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGly 454
Db 302 CAGGCTGGGAGGATTATCTTGTATTCGTATATGCAAGAGCAAGTAGGATAGCCACGGGT 361
QY 455 TyrLeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgPro 474
Db 362 TATCTGCCAACGTTTCGAGGAATACTTGGAGAACGGGAAAGTAGCTCTGGGCATCGCGTG 421
QY 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGlu 494
Db 422 TCGGCTTGCAACCCATGCTGACGATGGACATCCCCCTTCTCCTCACATCCTCAAGGAA 481

RESULT 12
CF477562/c
LOCUS
DEFINITION
RTWW3\_8\_G10.g1\_A022 Well-watered loblolly pine roots WW3 Pinus taeda cDNA clone RTWW3\_8\_G10\_A022 5', mRNA sequence.
ACCESSION
CF477562
VERSION
CF477562.1 GI:34506431
KEYWORDS
EST.
SOURCE
Pinus taeda (loblolly pine)
ORGANISM
Pinus taeda



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 740)  
Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.  
An EST database from well-watered loblolly pine (Pinus taeda) roots Unpublished (2003)  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: JENREV (CAGGAACACGCTATGACC).  
Location/Qualifiers  
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/organism="Pinus taeda"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3352"  
/clone="RTW3 8 G10\_A022"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WM3"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

FEATURES  
source

ORIGIN

Alignment Scores:  
Pred. No.: 2.14e-72 Length: 740  
Score: 723.00 Matches: 129  
Percent Similarity: 84.54% Conservative: 35  
Best Local Similarity: 66.49% Mismatches: 30  
Query Match: 22.24% Indels: 0  
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF477562 (1-740)

QY 425 GlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyr 444  
Db 739 CAAGGCTGGGATACAGTCAGCTATGCTCGAAATCTGGAGGCTTTTATTGGTGCTTAT 680  
QY 445 MetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGlu 464  
Db 679 ATACAAGAAGCCAAAGTGGATTTCAGTGTTATCTTCCACGTTCCGACGAGTACCTCGAG 620  
QY 465 AsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAsp 484  
Db 619 AATGGGAAGGTCAGCTCGGCTCTCGCATAAACCAGCTCGAACCCATGCTGACTTGGGG 560  
QY 485 IleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeu 504  
Db 559 TTTCTCTTCGCGCTCGAATCTGCAGGAAATTGACTTTCATCGAAATTCATGATTG 500  
QY 505 IleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArg 524  
Db 499 ATATGTGCCATCTTCGACTGAAGGTGACACTCAATGTACAAGGCTGACAGGCGCT 440  
QY 525 GlyGluGluAlaSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGlu 544

Db 439 GGAGAAGAAGCTTCGGCCGTATCGTGTATTATGAAAGACCACCTCTGGAATAACAGAGGAA 380  
QY 545 AspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGlu 564  
Db 379 GATGCTGTCAATCAAGTCAATGCTATGGTCGATACTTAACCAAGAACTGAATTGGGAG 320  
QY 565 LeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSer 584  
Db 319 TTACTTAGACCCGACAGCGGTGTCCCATCTCTTACAAGAAGGTGCTTTTGACATTTGC 260  
QY 585 ArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThr 604  
Db 259 AGAGTTTTCATTACGGTTACAATAACAGAGATGGCTTCAGTGTGCCAGTATTGAAATA 200  
QY 605 LysSerLeuValMetArgThrValIleGluProValProLeu 618  
Db 199 AAGAATTGGTAACAAGAACCGTGGTTGAAACTGTGCCTTTG 158

RESULT 13  
BQ698077  
LOCUS  
DEFINITION

BQ698077 516 bp mRNA linear EST 07-MAY-2003  
NXPV\_064\_C05\_F\_NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda  
cDNA clone NXPV\_064\_C05\_5' similar to Arabidopsis thaliana sequence  
At1g61680 hypothetical protein see  
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BQ698077.1 GI:21823393  
EST.  
Pinus taeda (loblolly pine)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Sederoff,R.  
Molecular Basis of Wood Formation in the Pine Megagenome  
Unpublished (2000)  
Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron\_sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further  
information.  
Seq primer: T3.

FEATURES  
source

1. .516  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXPV\_064\_C05"  
/tissue\_type="Xylem"  
/cell\_type="Planings (secondary)"  
/dev\_stage="Transitional"  
/lab\_host="Xli-Blue"  
/clone\_lib="NXPV (Nsf Xylem Planings wood Vertical)"  
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:  
XhoI; The library is from early (spring) secondary wood,  
taken from a ten year old tree in the transitional phase.  
The tree is a kind gift of the Westvaco Corporation.  
Secondary xylem was harvested from the tree by peeling  
back the bark and primary xylem and then removing the  
underlying tissue with a block plane. NOTE: The sequences  
contain a 'cDNA adapter' between the EcoRI site and the  
start of the EST. The adapter sequence is  
'AATTCGGCACGAG'."

ORIGIN

Alignment Scores:  
Pred. No.: 5.46e-72 Length: 516







GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 8, 2004, 16:55:46 ; Search time 786 Seconds  
(without alignments)  
3832.137 Million cell updates/sec

Title: US-10-025-145A-65  
Perfect score: 3251  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO\_spool/US10025145/runat\_07072004\_160150\_27970/app\_query.fasta\_1.775  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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ALIGNMENTS

RESULT 1  
US-10-025-145A-64  
; Sequence 64, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 64  
; LENGTH: 2013

1	3251	100.0	2013	15	US-10-025-145A-64	Sequence 64, Appl
2	2453	75.5	2018	9	US-09-887-586A-19	Sequence 19, Appl
3	2453	75.5	2018	9	US-09-903-012-19	Sequence 19, Appl
4	2453	75.5	2018	10	US-09-900-797-19	Sequence 19, Appl
5	2453	75.5	2018	13	US-09-893-820-19	Sequence 19, Appl
6	2453	75.5	2018	14	US-10-041-007-21	Sequence 21, Appl
7	2453	75.5	2018	15	US-10-025-145A-3	Sequence 3, Appli
8	2264	69.6	2186	15	US-10-025-145A-66	Sequence 66, Appl
9	2200.5	67.7	2196	9	US-09-887-586A-29	Sequence 29, Appl
10	2200.5	67.7	2196	9	US-09-903-012-29	Sequence 29, Appl
11	2200.5	67.7	2196	10	US-09-900-797-29	Sequence 29, Appl
12	2200.5	67.7	2196	13	US-09-893-820-29	Sequence 25, Appl
13	2200.5	67.7	2196	14	US-10-041-007-25	Sequence 1, Appli
14	2200.5	67.7	2196	15	US-10-025-145A-1	Sequence 31, Appl
15	2197.5	67.6	2205	15	US-10-025-145A-31	Sequence 77, Appl
16	2137	65.7	1890	15	US-10-025-145A-77	Sequence 27, Appl
17	2084.5	64.1	2429	14	US-10-041-007-27	Sequence 68, Appl
18	2084.5	64.1	2429	15	US-10-025-145A-68	Sequence 57, Appl
19	2031.5	62.5	2089	9	US-09-887-586A-57	Sequence 57, Appl
20	2031.5	62.5	2089	9	US-09-903-012-57	Sequence 57, Appl
21	2031.5	62.5	2089	10	US-09-900-797-57	Sequence 57, Appl
22	2031.5	62.5	2089	13	US-09-893-820-57	Sequence 57, Appl
23	2031.5	62.5	2089	14	US-10-041-007-23	Sequence 23, Appl
24	2031.5	62.5	2089	15	US-10-025-145A-5	Sequence 5, Appli
25	1295.5	39.8	1865	9	US-09-887-586A-47	Sequence 47, Appl
26	1295.5	39.8	1865	9	US-09-903-012-47	Sequence 47, Appl
27	1295.5	39.8	1865	10	US-09-900-797-47	Sequence 47, Appl
28	1295.5	39.8	1865	13	US-09-893-820-47	Sequence 47, Appl
29	1295.5	39.8	1865	14	US-10-041-007-17	Sequence 17, Appl
30	1250.5	38.5	1967	15	US-10-025-145A-17	Sequence 17, Appl
31	1240.5	38.2	2700	9	US-09-887-586A-43	Sequence 43, Appl
32	1240.5	38.2	2700	9	US-09-903-012-43	Sequence 43, Appl
33	1240.5	38.2	2700	10	US-09-900-797-43	Sequence 43, Appl
34	1240.5	38.2	2700	12	US-10-041-018-363	Sequence 363, App
35	1240.5	38.2	2700	13	US-09-893-820-43	Sequence 43, Appl
36	1231	37.9	1785	9	US-09-887-586A-49	Sequence 49, Appl
37	1231	37.9	1785	9	US-09-903-012-49	Sequence 49, Appl
38	1231	37.9	1785	10	US-09-900-797-49	Sequence 49, Appl
39	1231	37.9	1785	13	US-09-893-820-49	Sequence 49, Appl
40	1231	37.9	1785	14	US-10-041-007-19	Sequence 19, Appl
41	1187	36.5	2424	9	US-09-887-586A-45	Sequence 45, Appl
42	1187	36.5	2424	9	US-09-903-012-45	Sequence 45, Appl
43	1187	36.5	2424	10	US-09-900-797-45	Sequence 45, Appl
44	1187	36.5	2424	13	US-09-893-820-45	Sequence 45, Appl
45	1187	36.5	2424	14	US-10-041-007-14	Sequence 14, Appl

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; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(1889)
; OTHER INFORMATION:
US-10-025-145A-64

Alignment Scores:
Pred. No.: 0 Length: 2013
Score: 3251.00 Matches: 618
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-025-145A-65 (1-618) x US-10-025-145A-64 (1-2013)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeuSerSerHisGlu 20
Db 36 ATGGCTCTTCTTCTATTAATCCGCTGGTTCCAGGTCGTGCCTCAGTTCTTCTCATGAG 95
QY 21 IleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArgProGlyLysSerVal 40
Db 96 ATTAAGGCTCTCCGTAGAACAAATCCCAACTCTTGAATCTGCAGGCCGGGAAATCCGTC 155
QY 41 AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg 60
Db 156 GCGCATTCATAAAACATGTGTTTGACAAAGCGTCGCATCTACTGATTCGTACAGAGACGC 215
QY 61 ValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGlnSerLeuIleSerThr 80
Db 216 GTGGGCAACTATCAATTCCAACTGTGGGACGATGATTTTCATACAGTCTCTGATCTCAACG 275
QY 81 ProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyGluValLysAsp 100
Db 276 CCTTATGGAGCACCTGATTACCGGGAACGTCGTGACAGACTTATTGGGGAAGTAAAGGAT 335
QY 101 IleMetPheAsnPhelysSerLeuGluAspGlyGlyAsnAspLeuLeuGlnArgLeuLeu 120
Db 336 ATAATGTTCAATTTCAAGTCGCTGGAAGATGGAGGCAATGATCTCCTTCAACGACTTTTG 395
QY 121 LeuValAspAspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThr 140
Db 396 CTGGTCGATGACGTTGAACGTTTGGGAATCGACAGGCATTTCAAAAAGAGATAAAAACG 455
QY 141 AlaLeuAspTyrValAsnSerTyrTrpAsnGluLysGlyIleGlyCysGlyArgGluSer 160
Db 456 GCACCTCGATTATGTTAAAGTTATTGGAAACGAAAAGGCATTTGATGTGGGAGGAGAGT 515
QY 161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr 180
Db 516 GTTGTGACTGACCTCAACTCAACCGCCTTGGGGCTTCGAACTCTCCGACTACACGGATAC 575
QY 181 ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr 200
Db 576 ACTGTGCTTTCAGATGTTTGAACGTTTTTAAAGACAAAAAATGGGCAATTTTTCCTCCACT 635
QY 201 AlaAsnIleGlnIleGluGlyGluIleArgGlyValLeuAsnLeuPheArgAlaSerLeu 220
Db 636 GCCAATATTCCAGATAGAGGGAGAGATTAGAGGCGTTCTCAATTTATTTCAGGGCCTCCCTC 695
QY 221 ValAlaPheProGlyGluLysValMetAspGluAlaGluThrPheSerThrLysTyrLeu 240
Db 696 GTCCCTTTCCCGCGAGAAAGTTATGGATGAAGCTGAAACATTTCTACAAAAATATTA 755
QY 241 ArgGluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal 260
Db 756 AGAGAAAGCCCTGCAAAAGATTCCGGCATCCAGTATACITTCCTAGAGATACGGGACGTT 815
QY 261 LeuGluTyrGlyTrpHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal 280
Db 816 CTGGAATATGTTGGCACACCAATTTGCCACGCTTGGAAAGCAAGGAATTACATGGACGTC 875
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QY 281 PheGlyGlnHisThrLysAsnLysAsnAlaAaGluLysLeuLeuGluLeuAlaLysLeu 300
Db 876 TTTGGACAGCACACTAAAATAAGAACGCGCCGAGAAACCTTTTAGAACTTGCAAAATTG 935
QY 301 GluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrp 320
Db 936 GAATTCATATATTTCACTCCTTACAAGAGAGAGAGTTAAAACATGTTCCTCGATGGTGG 995
QY 321 LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla 340
Db 996 AAAGACTCGGGTTCTCTGAGATGACCTTCTGTGACATCGTCACTGGAATACTACGCT 1055
QY 341 LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLys 360
Db 1056 TTGGCTTCCTGCATTGCGTTTCGAGCTCAACATTTCTGGATTTCAGACTCGGCTTTACCAAG 1115
QY 361 MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu 380
Db 1116 ATGTCTCATCTTATCACGGTTCTTTCAGACATGTACGACGTCTTCGGCACAGTAGACGAG 1175
QY 381 LeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuPro 400
Db 1176 CTGGAACCTCTTCACAGCGACAATTAAGAGATGGGATCCGTCCGCGATGGAATGCCTTCCA 1235
QY 401 GluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal 420
Db 1236 GAATATATGAAGGAGGTGTACATGATGGTTTATCACACCGTAAATGAATGGCTCGAGTG 1295
QY 421 AlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCys 440
Db 1296 GCAGAGAAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGT 1355
QY 441 PheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlu 460
Db 1356 TTTGATTTCGTATATGCAGGAAGCAAAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAG 1415
QY 461 GluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
Db 1416 GAGTACTTGGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATT 1475
QY 481 LeuThrLeuAspIlePropheProAspHisIleLeuLysGluValAspPheProSerLys 500
Db 1476 CTGACGTTGGACATCCCTTTCTCTGATCACATCTCAAGGAAGTTGACTTCCCATCGAAG 1535
QY 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAla 520
Db 1536 CTCAATGACTTGTATGTATCATCTTTCGATTAAAGAGGTGATACACGGTGTCTACAAGGCA 1595
QY 521 AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGly 540
Db 1596 GACAGGGCCCGTGGAGAAAGAAAGCTTCGTCTATATATCATGTTATATGAAAGACAATCCTGGA 1655
QY 541 LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu 560
Db 1656 TTAACGGAAGAAGATGCTCTGAATCATATCAACITTCATGATCAGGGACGCAATCAGAGAA 1715
QY 561 LeuAsnTrpGluLeuLysProAspAsnSerValProIleThrSerLysLysHisAla 580
Db 1716 TTAAATTGGGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCACTTCCAAGAAACACCGCA 1775
QY 581 PheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAla 600
Db 1776 TTTGACATAAGCAGAGTTTGGCATCACGGTTTACAGATACCGAGATGGCTACAGCTTTGCC 1835
QY 601 AsnValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1836 AACGTTGAACAAAGAGTTTGGTGTGATGAGAACCCGTCACTGAACCTGTGCCTTTG 1889
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RESULT 2  
US-09-887-586A-19  
; Sequence 19, Application US/09887586A  
; Patent No. US20020094556A1



; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-887-586A-19

Alignment Scores:
Pred. No.: 8,09e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 9 Gaps: 6

US-10-025-145A-65 (1-618) x US-09-887-586A-19 (1-2018)

QY	1	MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu-----	15
Db	6	ATGGCTCTAGTTTACCGCACCGTTGGCTTCCAAATCATGCCTGCACAAATCGTTGATC	65
QY	16	SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg	35
Db	66	AGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAAATCCAGCTCTAGGAATGAGTAGG	125
QY	36	ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp	55
Db	126	CGAGGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACCGTTGTAAACCGATGAT	185
QY	56	SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln	75
Db	186	GGTGACGAAGACGCATGGCGGATTTCCATTCCAACCTCTGGGACGATGATGTACATACAG	245
QY	76	SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle	95
Db	246	TCCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGTGAGAAACTGATC	302
QY	96	GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly-----	112
Db	303	GGGGAAGTAAAGAAC---ATGTTCAATTTCGATGTCAATAGAGATGGAGAGTTAATGAGT	359
QY	113	-----AsnAspLeuLeuGlnArgLeuLeuLeuValAspValGluArgLeuGlyIle	130
Db	360	CCGCTCAATGATCTCATTCACACGCCCTTTGGATTGTCGACAGCCTTGAACGTTTGGGGATC	419
QY	131	AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn	150
Db	420	CATAGACATTTCAAAGATGAGATAAAATCGCGCTTGATTATGTTTACAGTTATTGGGGC	479
QY	151	GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu	170
Db	480	GAAATGGCATCGGATCGGGAGGGAGAGTGTGTGTACTGATCTGAACTCAACTCGCGTTG	539

QY	171	GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe	190
Db	540	GGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTTCAAAGCTTTC	599
QY	191	LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg	210
Db	600	AAAGGCCAAATGGGCAGTTTTCTCTGCTCTGAAATATTCAGACAGATGAAGAGATCAGA	659
QY	211	GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp	230
Db	660	GGCGTTCGAATTTATTCGGGCCCTCCCTCAITGGCTTTCAGGGGAGAAAAATTATGGAT	719
QY	231	GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer	250
Db	720	GAGGCTGAAATCTTCTTACCAATATTTAAAGAACCCCTGCAAAAGATTCCGCTCTCC	779
QY	251	SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro	270
Db	780	AGT---CTTTCGCGAGAGATCGGGACGTTTTTGAATATGTTGGCACACATATTGCGG	836
QY	271	ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla	290
Db	837	CGATTGGAAGCAAGGAATTACATCCAAGTCTTTGGACAGGACACTGAGAACACGAAAGTCA	896
QY	291	-----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer	307
Db	897	TATGTGAAGAGCAAAAACTTTTAGAACTCGCAAAATTTGGAGTTCAACATCTTCAATCC	956
QY	308	LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu	327
Db	957	TTACAAAAGAGGGAGTTAGAAAGTCTGGTTCAGATGGTGGAAAGAAATCGGGTTTTCTGAG	1016
QY	328	MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe	347
Db	1017	ATGACCTTCTGCCGACATCGTCACGTGGAACTACTACACTTTGGCTTCCCTGCATTGCGTTC	1076
QY	348	GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal	367
Db	1077	GAGCCTCAACATTTCTGGATTCAGACTCGGCTTTGCCAAGACGTGTCTATCTTATCAGGTT	1136
QY	368	LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr	387
Db	1137	CTTGACGATATGTACGACACCTTCGGCACACTAGACGAGCTGGAACTCTTCACAGCGACA	1196
QY	388	IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr	407
Db	1197	ATGAAGAGATGGGATCCGTCCTTCGATAGATTGCCTTCCAGAATATATGAAGGAGTGTAC	1256
QY	408	MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg	427
Db	1257	ATAGCGGTTACGACACCGTAAATGAAATGGCTCGAGAGGCAGAGAGGCTCAAGGCCGA	1316
QY	428	AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu	447
Db	1317	GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTCTGTATATGCAAGAA	1376
QY	448	AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys	467
Db	1377	GCAAGGTGGATCGCCACTGGTTTACCTGCCCTCCTTTGATGAGTACTACGAGAATGGGAAA	1436
QY	468	ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe	487
Db	1437	GTTAGCTGTGTCATCGCATATCCGCATTTGCAACCCATTCTGACAAATGGACATCCCCCTT	1496
QY	488	ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle	507
Db	1497	CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCCTTAACGACTTGGCATGTGCC	1556
QY	508	IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu	527
Db	1557	ATCCTTCGATTACGAGGTGATACCGCGGTGCTACAAAGCGGACAGGGCTCGTGGAGAAGAA	1616
QY	528	AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu	547

Db 1617 GCTTCCTCTATATCATGTTATATGAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676  
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567  
Db 1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAATTTGGGAACCTTCTCAA 1736  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587  
Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796  
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607  
Db 1797 CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAGAGTTTG 1856  
QY 608 ValMetArgThrValIleGluProValProLeu 618  
Db 1857 GTCACGAGAACCTCCTTGAATCTGTGCCTTTG 1889

RESULT 3

US-09-903-012-19  
; Sequence 19, Application US/09903012  
; Patent No. US20020094557A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094557A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/903,012  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,993  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 2018  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)...(1889)  
; OTHER INFORMATION: pinene synthase  
US-09-903-012-19

Alignment Scores:  
Pred. No.: 8.09e-279 Length: 2018  
Score: 2453.00 Matches: 475  
Percent Similarity: 84.63% Conservative: 59  
Best Local Similarity: 75.28% Mismatches: 81  
Query Match: 75.45% Indels: 16  
DB: 9 Gaps: 6

US-10-025-145A-65 (1-618) x US-09-903-012-19 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
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QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCTAGGAATGAGTAGG 125  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 126 CGAGGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCAACCGTTGTAAACCGATGAT 185

QY 56 SerValGlnArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75  
Db 186 GGTGTACGAAGACGCATGGCGGATTTCCATTCCAACCTCTGGGACGATGATGTATACAG 245  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGCTGAGAAACTGATC 302  
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 303 GGGGAAGTAAAGAAC---ATGTTCAATTCGATGTCATTAGAAGATGGAGAGTTAATGAGT 359  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuLeuValAspValGluArgLeuGlyIle 130  
Db 360 CCGCTCAATGATCTCATTCACGCGCTTTGGATTGTCGACAGCCTTGAACGTTTGGGGATC 419  
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
Db 420 CATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATGTTTACAGTTATTGGGC 479  
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 480 GAAAATGGCATCGGATCGGGAGGAGAGTGTTGTACTGATCTGAACCTCAACTGCGTTG 539  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 540 GGGCTTCGAACCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTTCAAGCTTTC 599  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
Db 600 AAAGGCCAAAATGGGCAGTTTTCTGCTCTGAAAATATTTCAGACAGATGAAGAGATCAGA 659  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 660 GCGGTTCTGAATTTATTCGGGCGCTCCCTCATTTGCTTCCAGGGGAGAAAATATGGAT 719  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 720 GAGGCTGAAATCTTCTACCAATAATTTAAAAGAGCCCTGCAAAAGATTCCGGTCTCC 779  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270  
Db 780 AGT---CTTTCCGAGAGATCGGGACGTTTTTGAATATGTTGGCACACATATTTGCCG 836  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290  
Db 837 CGATTGGAAGCAAGGAATTACATCCAAGTCTTTGGACAGGACACTGAGAACACCAAGTCA 896  
QY 291 -----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307  
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QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327  
Db 957 TTACAAAAGAGGGAGTTAGAAAAGTCTGGTCAGATGGTGGAAAAGAAATCGGGTTTTCTGAG 1016  
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
Db 1017 ATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTGGCTTTCCTGCTTGGCTTC 1076  
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
Db 1077 GAGCCTCAACATTTCTGGATTTCAGACTCGGCTTTGCCAAGACGCTGTATCTTATCAGGTT 1136  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387  
Db 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACCTTTCACAGCGACA 1196  
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
Db 1197 ATGAAGAGATGGGATCCGTCCTCGATAGATTGGCTTCCAGAAATATATGAAGGAGTGTAC 1256

QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427  
Db 1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCAGAGGAGGCTCAAGGCCGA 1316  
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447  
Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATTGATTTCGTATATGCAAGAA 1376  
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
Db 1377 GCAAGGTGGATCGCCACTGGTTACCTGCCCTCCTTTGATGAGTACTACGAGAATGGGAAA 1436  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIlePropHe 487  
Db 1437 GTTAGCTGTGGTATCGCATATCCGCAATTGCAACCCATTCTGACAATGGACATCCCTTT 1496  
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
Db 1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCTTAACGACTTGGCATGTGCC 1556  
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527  
Db 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAA 1616  
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547  
Db 1617 GCTTCCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676  
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567  
Db 1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAAATTGGGAACCTTCTCAA 1736  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587  
Db 1737 CCAGACATCAATGTTCCTCATCTCGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796  
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607  
Db 1797 CATTAACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG 1856  
QY 608 ValMetArgThrValIleGluProValProLeu 618  
Db 1857 GTCACGAGAACCTCCTTGAATCTGTGCGCTTG 1889

RESULT 4

US-09-900-797-19  
; Sequence 19, Application US/09900797  
; Publication No. US20030087406A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20030087406A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/900,797  
; CURRENT FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: US/09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 2018  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)...(1889)  
; OTHER INFORMATION: pinene synthase

US-09-900-797-19  
Alignment Scores:  
Pred. No.: 8.09e-279 Length: 2018  
Score: 2453.00 Matches: 475  
Percent Similarity: 84.63% Conservative: 59  
Best Local Similarity: 75.28% Mismatches: 81  
Query Match: 75.45% Indels: 16  
DB: 10 Gaps: 6  
US-10-025-145A-65 (1-618) x US-09-900-797-19 (1-2018)  
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
Db 6 ATGGCTCTAGTTTCTACCGCACCGTTGGCTTCCAATCATGCCTGCACAAATCGTTGATC 65  
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCTAGGAATGAGTAGG 125  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 126 CGAGGGAATCTATCACTCTCTCCATCAGCATGAGCTTACCACCGTTGTAAACCGATGAT 185  
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75  
Db 186 GGTGTACGAAGACGATGGCGGATTTCCATTCCAACCTCTGGACGATGATGTATACATACAG 245  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGTGAGAAACTGATC 302  
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 303 GGGGAAGTAAAGAAC---ATGTTCAATTTCGATGTCATTAGAAGATGGAGAGTTAATGAGT 359  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuLeuValAspAspValGluArgLeuGlyIle 130  
Db 360 CCGCTCAATGATCTCATTCACGCGCTTTGGATTGTTCGACAGCCTTGAAACGTTTGGGGATC 419  
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
Db 420 CATAGACATTTCAAAGATGAGATAAAATCGCGCTTGATTATGTTACAGTTATTGGGCGC 479  
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 480 GAAATGGCATCGGATGCGGGAGGGAGAGTGTTGTTACTGATCTGAACCTCAACTGCGTTG 539  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 540 GGGCTTCGAACCCCTACGACTACCGGATACCGGATACCGGTGTCTTCAGATGTTTCAAAGCTTTC 599  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
Db 600 AAAGGCCAAAATGGGCAGTTTTCTCGCTCTGAAAATATTTCAGACAGATGAAGAGATCAGA 659  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 660 GCGCTTCTGAATTATTCCGGGCGCTCCCTCATTTGCCCTTTCAGGGGAGAAAAATTATGGAT 719  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 720 GAGGCTGAAATCTTCTCTACCAAAATATTTAAAGAACGCCCTGCAAAAGATTCCGGTCTCC 779  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270  
Db 780 AGT---CTTTCCGAGAGATCGGGGACGTTTGTGGAATATGTTGGCACACATATTTGCCG 836  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290  
Db 837 CGATTGGAAGCAAGGAATTACATCCAAGTCTTTGGACAGACACTGAGAACACCGAAGTCA 896  
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307



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Db      897  TATGTGAAGAGCAAAAAACCTTTAGAACTCGAAAAATTGGAGTTCAACATCTTTCAATCC 956
QY      308  LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db      957  TTACAAAAGAGGGAGTTAGAAAGTCTGGTCAGATGGTGGAAGAATCGGGTTTTCCTGAG 1016
QY      328  MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db      1017 ATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTGGCTTCCTGTCATTCGTTT 1076
QY      348  GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db      1077 GAGCCTCAACATTCTGGATTTCAGACTCGGCTTTGCCAAGACGTTGTCATCTTATCACGGTT 1136
QY      368  LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db      1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAATCTTTCACAGCGACA 1196
QY      388  IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db      1197 ATGAAGAGATGGATCCGTCCTCGATAGATTGCCTTCAGAAATATATGAAAGGAGTGTAC 1256
QY      408  MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db      1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCAGAGGCTCAAGGCCGA 1316
QY      428  AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db      1317 GATACGCTCACATATGCTCGGAAGCTTGGAGGCTTATATTGATTCGTATATGCAAGAA 1376
QY      448  AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db      1377 GCAAGGTGGATCGCCACTGGTTACCTGCCCTTCCTTTGATGAGTACTACGAGAATGGAAA 1436
QY      468  ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProphe 487
Db      1437 GTTAGCTGTGGTCATCGCATATCCGCATTGCAACCCATTCTGACAAATGGACATCCCTTT 1496
QY      488  ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db      1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAAGCTTAACGACTTGGCATGTGCC 1556
QY      508  IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db      1557 ATCCTTCGATTACGAGGTGATACGCGGTGCTACAAGCGGACAGGGCTCGTGGAGAAGAA 1616
QY      528  AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db      1617 GCTTCTCTATATCATGTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676
QY      548  AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db      1677 GATCATATCAACGCCATGATCAGTGACGTAATCAAAGGATTAATTTGGGAACITTCIAAA 1736
QY      568  ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db      1737 CCAGACATCAATGTTCCCATCTCGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796
QY      588  HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db      1797 CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAAGCTTGAAACGAAGAGTTTG 1856
QY      608  ValMetArgThrValIleGluProValProLeu 618
Db      1857 GTCACGAGAACCCTCCTTGAATCTGTGCCTTTG 1889
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RESULT 5

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US-09-893-820-19
; Sequence 19, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
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; APPLICANT: No. US20040053386All, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
; US-09-893-820-19
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Pred. No.:      8.09e-279      Length:      2018
Score:          2453.00        Matches:    475
Percent Similarity: 84.63%    Conservative: 59
Best Local Similarity: 75.28%  Mismatches:  81
Query Match:      75.45%      Indels:     16
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US-10-025-145A-65 (1-618) x US-09-893-820-19 (1-2018)

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QY     16  SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db     66  AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCTAGGAATGAGTAGG 125
QY     36  ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db    126  CGAGGGAAATCTATCACTCCTTCCATCAGCATGAGCTTACCACCGTTGTAAACCGATGAT 185
QY     56  SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db    186  GGTGTACGAAGACGATGGGCGATTTCATTTCCAACTCTGGGACGATGATGTCTATACAG 245
QY     76  SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db    246  TCTTTA---CCAAACGGCTTATGAGGAAAAATTCGTACTGGAGCGTGTGAGAAACTGATC 302
QY     96  GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db    303  GGGGAAGTAAAGAAC---ATGTTCAATTTCGATGTCTATTAGAAGATGGAGATTAATGAGT 359
QY    113  -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db    360  CCGCTCAATGATCTCATTTCAACGCCCTTTGGATTGTTCGACAGCCTTGAACGTTTGGGGATC 419
QY    131  AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db    420  CATAGACATTTCAAAGATGAGATAAAATCGGCGCTTGATTATGTTTACAGTTATTGGGCG 479
QY    151  GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db    480  GAAATGGCATCGGATCGGGGAGGAGAGAGTGTGTTGTTACTGATCTGAACCTCAACTCGCTTG 539
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QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 540 GGGCTTCGAACCCCTACGACTACACGGATACCCGGTGCTTCAGATGTTTTCAAAGCTTTC 599  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
Db 600 AAAGGCCAAAATGGGCAGTGTTCCTGCTCTGAAATATTCAGACAGATGAAGAGATCAGA 659  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 660 GGGCTTCTGAATTTATTCGGGCCTCCCTCATTTGCCCTTCCAGGGGAGAAAATTATGGAT 719  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 720 GAGGCTGAAATCTTCTTACCAAATATTTAAAGAAGCCCTGCAAAAGATTCCGGTCTCC 779  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270  
Db 780 AGT---CTTTCGCGAGAGATCGGGACGTTTTTGGAAATATGTTGGCACACATATTGCCG 836  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290  
Db 837 CGATTGGAAGCAAGGAATTACATCCAAGTCTTTGGACAGGACACTGAGAACACGAAGTCA 896  
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307  
Db 897 TATGTGAAGAGCAAAAAAATTTAGAACTCGCAAAATGGAGTTCAACATCTTTCAATCC 956  
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327  
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QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
Db 1017 ATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTGGCTTCCCTGCATTCGCTTC 1076  
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
Db 1077 GAGCCTCAACATCTGGATTTCAGACTCGGCTTGGCAAGACGCTGTCTATCATCACGGTT 1136  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387  
Db 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACCTTTCACAGCGACA 1196  
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
Db 1197 ATGAAGAGATGGGATCCGTCCTCGATAGATTGCCTTCCAGAAATATATGAAGGAGTGTAC 1256  
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427  
Db 1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCGAGAGGCTCAAGGCCGA 1316  
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447  
Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTTCGTATATGCAAGAA 1376  
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
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QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
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Db 1617 GCTTCCTCTATATCATGTATATGAAAGACAAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676  
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Db 1677 GATCATATCAACGCCCATGATCAGTGACGTAATCAAAAGGATTAAATTTGGAACTTCTCAAA 1736  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587  
Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796  
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607  
Db 1797 CATACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG 1856  
QY 608 ValMetArgThrValIleGluProValProLeu 618  
Db 1857 GTCACGAGAACCCCTCCTTGAATCTGTGCCCTTG 1889  
RESULT 6  
US-10-041-007-21  
; Sequence 21, Application US/10041007  
; Publication No. US20020164736A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsuda, Seiichi P.T.  
; APPLICANT: Schepmann, Hala G  
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase  
; FILE REFERENCE: P02081US1  
; CURRENT APPLICATION NUMBER: US/10/041,007  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: US 60/259,881  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 2018  
; TYPE: DNA  
; ORGANISM: Abies grandis  
US-10-041-007-21  
Alignment Scores:  
Pred. No.: 8.09e-279 Length: 2018  
Score: 2453.00 Matches: 475  
Percent Similarity: 84.63% Conservative: 59  
Best local Similarity: 75.28% Mismatches: 81  
Query Match: 75.45% Indels: 16  
DB: 14 Gaps: 6  
US-10-025-145A-65 (1-618) x US-10-041-007-21 (1-2018)  
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
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QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAATTCCAGCTCTAGGAATGAGTAGG 125  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 126 CGAGGGAATCTATCACTCTCTCCATCAGCATGAGCTCTACCACCGTTGTAAACCGATGAT 185  
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75  
Db 186 GGTGTACGAAGACGCATGGCGGATTTCCATTCCAAACCTCTGGGACGATGATGTATACAG 245  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGTGAGAAACTGATC 302  
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 303 GCGGAAGTAAAGAAC---ATGTTCAATTTCGATGTCATTAGAAGATGGAGAGTTAATGAGT 359

QY	113	-----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle	130
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QY	131	AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn	150
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QY	151	GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu	170
Db	480	GAAATGGCATCGGATCGGGAGGAGAGTGTGTTACTGATCTGAACTCAACTGCGTTG	539
QY	171	GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe	190
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QY	191	LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg	210
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QY	211	GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp	230
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QY	231	GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer	250
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Db	780	AGT---CTTTCCGAGAGATCGGGACGTTTTTGGAAATATGTTGGCACACATATTTCGGC	836
QY	271	ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla	290
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QY	291	-----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer	307
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QY	308	LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu	327
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QY	328	MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe	347
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QY	348	GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal	367
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QY	368	LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr	387
Db	1137	CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACCTCTTCACAGCGACA	1196
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Db	1257	ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGACAGGAGGCTCAAGGCCGA	1316
QY	428	AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu	447
Db	1317	GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATTGATTTCGTATATGCAAGAA	1376
QY	448	AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys	467
Db	1377	GCAAGGTGGATCGCCACTGTTTACCTGCCCTCTTGTGATGAGTACTACGAGAATGGGAAA	1436
QY	468	ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe	487
Db	1437	GTTAGCTGTGGTCATCGCATATCCGATTTGCAACCCATTTCTGACAATGGACATCCCCITT	1496
QY	488	ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle	507
Db	1497	CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAAGCTTAACGACTTGGCATGTGCC	1556
QY	508	IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaAargGlyGluGlu	527
Db	1557	ATCCTTCGATTACGAGGTGATACCGGCTGTCTACAAGCGGACAGGGCTCGTGGAGAAGAA	1616
QY	528	AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu	547
Db	1617	GCTTCTCTATATCATGTTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTCTC	1676
QY	548	AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys	567
Db	1677	GATCATATCAACGCCCATGATCAGTGACGTAATCAAAGGATTAATTGGGAACCTTCTCAA	1736
QY	568	ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp	587
Db	1737	CCAGACATCAATGTTCCCATCTCGCGGAAGAAAATCATGCTTTTGACATCGCCAGAGCTTC	1796
QY	588	HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu	607
Db	1797	CATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTTGAAACGAAGAGTTTG	1856
QY	608	ValMetArgThrValIleGluProValProLeu	618
Db	1857	GTCACGAGAACCTCCTTGAATCTGTGCCTTTG	1889
RESULT 7			
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; Sequence 3, Application US/10025145A			
; Publication No. US20030175861A1			
; GENERAL INFORMATION:			
; APPLICANT: Croteau, Rodney B.			
; APPLICANT: Bohlmann, Joerg			
; APPLICANT: Steele, Christopher L.			
; APPLICANT: Phillips, Michael A.			
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)			
; FILE REFERENCE: WSUR118414			
; CURRENT APPLICATION NUMBER: US/10/025,145A			
; CURRENT FILING DATE: 2002-06-28			
; PRIOR APPLICATION NUMBER: US 09/360,545			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: PCT/US98/14528			
; PRIOR FILING DATE: 1998-07-10			
; PRIOR APPLICATION NUMBER: US 60/052,249			
; PRIOR FILING DATE: 1997-07-11			
; NUMBER OF SEQ ID NOS: 107			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 3			
; LENGTH: 2018			
; TYPE: DNA			
; ORGANISM: Abies Grandis			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (6)..(1892)			
; OTHER INFORMATION:			
US-10-025-145A-3			
Alignment Scores:			
Pred. No.:	8.09e-279	Length:	2018
Score:	2453.00	Matches:	475
Percent Similarity:	84.63%	Conservative:	59
Best Local Similarity:	75.28%	Mismatches:	81
Query Match:	75.45%	Indels:	16
DB:	15	Gaps:	6
US-10-025-145A-65 (1-618) x US-10-025-145A-3 (1-2018)			

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
Db 6 ATGCGCTAGTTTCTAACCACCGCTTGCGTCCAAATCATGCCCTGCACAAATCGTTGATC 65  
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35  
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QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112  
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTGATGTCTATTAGAAGATGAGAGTTAATGAGT 359  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130  
Db 360 CCGCTCAATGATCTCATTCACAACGCTTTGGATGTGCACAGCCTGAACGTTGGGATC 419  
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
Db 420 CATAGACATTTCAAGATGAGATAAATCGCGCTTGATTTATGTTCAGATTATTGGGGC 479  
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 480 GAAATATGGCATCGGATCGGGAGGAGAGTGTGTTACTGATCTGAACCTCAACTGCGGTG 539  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 540 GGGCTTCGAACCTACGACTACACGGAATACCGGTGTCTTACAGATTTTCAAGCTTTC 599  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLysLeuArg 210  
Db 600 AAAGGCCAAATGGGAGTTTCTGCTCTGAAATATTCAGACAGATGAAGAGATCAGA 659  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
Db 660 GCGCTTCGAATTTATTCGGGCTCCTCATTCGCTTCCAGGGAGAAAAATTATGAT 719  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 720 GAGGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCACAAAAGATTCCGGTCTCC 779  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270  
Db 780 AGT---CTTTCGGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTGGCCG 836  
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290  
Db 837 CGATTGGAAGCAAGGAATTACATCAAGTCTTTGGACAGACACTGAGAACACGAAAGTCA 896  
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307  
Db 897 TATGTGAAGAGCAAAAAAATTGAACTCGCAAAATTGAGTTCAACATCTTCAATCC 956  
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327  
Db 957 TTACAAAAAGAGGAGTAGAAAGTCTGCTCAGATGCTGGAAGAAGATCGGGTTTCCGTAG 1016  
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347  
Db 1017 ATGACCTTCTGCGACATCGTACGTGGAATACTACACTTTGGCTTCTGCAATGCGCTTC 1076  
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367

Db 1077 GAGCTCAACATTTCTGATTCAGACTCGGCTTTGCCAAGACGTGTGATCTTATCACGGTT 1136  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387  
Db 1137 CTTCAGCATATGTAACGACACCTTCGGCACAGTAGACGAGCTGGAATCTTTCACAGCGACA 1196  
QY 388 IleLysArgTyrPaspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
Db 1197 ATGAAGAGATGGATCCGCTCCCTCGATAGATTGCCCTTCCAGAAATATATGAAGAGGTAC 1256  
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427  
Db 1257 ATAGCGGTTTACGACACCGTAAATGAATGGCTCGAGAGCGAGAGGCTCAAGGCCGA 1316  
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447  
Db 1317 GATACGCTACATATGCTCGGGAAGCTTGGAGGCTTATATTGATTGATTGATATGCAAGAA 1376  
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
Db 1377 GCAAGGTGATGCCCACTGTTACCTGCCCTCTTGATGAGTACTACAGAAATGGGAAA 1436  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487  
Db 1437 GTTAGCTGTGTCATCGCATATCCGCAATTGCAACCATTTGTGACAAATGACATCCCTTT 1496  
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
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QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527  
Db 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTACAAAGCGGACAGGGCTCTGAGAGAA 1616  
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547  
Db 1617 GCTTCTCTATATCATGTTATATGAAGAACAAATCCTGAGTATCAGAGAAAGATGCTCTC 1676  
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567  
Db 1677 GATCATATCAACGCCATGATCAGTACGTAATCAAAAGATTAATGGGAATCTCTCAA 1736  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTyr 587  
Db 1737 CCAGACATCAATGTTCCCATCTCGGGCAAGAAACATGCTTTTGACATCCGACAGCTTTC 1796  
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607  
Db 1797 CATACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAGAAAGATTGG 1856  
QY 608 ValMetArgThrValIleGluProValProLeu 618  
Db 1857 GTCACGAGAACCTCCTTGATCTGTGCTTTG 1889  
  
RESULT 8  
US-10-025-145A-66  
; Sequence 66, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249



; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1923)
; OTHER INFORMATION:
US-10-025-145A-66

Alignment Scores:
Pred. No.: 1.97e-256 Length: 2186
Score: 2264.00 Matches: 435
Percent Similarity: 80.53% Conservative: 78
Best Local Similarity: 68.29% Mismatches: 98
Query Match: 69.64% Indels: 26
DB: 15 Gaps: 9

US-10-025-145A-65 (1-618) x US-10-025-145A-66 (1-2186)

QY 1 MetAlaleuSerleThrProLeuValSerArgSerCysLeu----- 15
Db 34 ATGCTCTGTTCTTCCGACCC-----AAATCCTGCTGCACAAATCGTTGATC 84
QY 16 ---SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCys 34
Db 85 AGGTCTACTCATCATGAGCTCAAGCCTCTGCGAGAACCATCCCAACTCTTGAATGTGT 144
QY 35 ArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr 54
Db 145 AGCGCGAGGAAATCTTTCACACCTTCTGTGAGCATGAGTTTGACCAACCGCTGATCTGAT 204
QY 55 AspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrPaspAspPheIle 74
Db 205 GATGCTCTACAAAGACGATAGGTGATCATTCATTCATCTCTGGAGACGACGATTTCATA 264
QY 75 GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluAlaAspArgLeu 94
Db 265 CAGTCTCTA---TCAACGCCCTTATGGGAGCCTTCTTACCGAGAACGTGCTGAGAAACTG 321
QY 95 IleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 322 ATTGGGGAAGTGAAGAG---ATGTTCAATTCAATGCCATCGAAGATGAGAATCAATG 378
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
Db 379 AGTCCCTCATGATCTTATTTGAACGACTTTGGATGGATGCGATAGCGTTGAACGTTTGGGG 438
QY 130 IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrp 149
Db 439 ATTGATAGACATTTCAAAAAAGAGATAAAATCAGCCCTTGATATGTTTACAGTATTGG 498
QY 150 AsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
Db 499 AAGGAAAAAGGTATTGGATGCGGTAGAGATAGTGTTTTCTCGATGTCACTCGACTGCC 558
QY 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnVal 189
Db 559 TCGGGGTTTCGAACCTCTTCGCTTACACGAGATACAGTGTCTCTTCAGAGGTTTGAAGTA 618
QY 190 PheLysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIle 209
Db 619 TTTCAGAGACCAAAATGGGCAGTTTGCAATCTCTCCTAGTACAAAA--GAGAGAGACATC 675
QY 210 ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMet 229
Db 676 AGAACCGTCTCGAATTATATCGGGCTTCTTTCATTTGCTTCTCGGGGAGAAAGTTATG 735
QY 230 AspGluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAla 249

Db 736 GAAGAGCGCTGAAATTTTCTCTTCAAGATATTTGAAAGAGCCGTCGAAAAAGATTCCGGTC 795
QY 250 SerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPHisThrAsnLeu 269
Db 796 TCCAGT---CTTTCACAAGAAATAGACTACACTTTGGAAATATGTTGGCACACAAATATAG 852
QY 270 ProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThr----- 285
Db 853 CCAAGATTGGAACAAGAAATTACTTAGATGATTTTGACATCTTACCAGTCCATGGCTC 912
QY 286 LysAsnLysAsnAla-----AlaGluLysLeuLeuGluLeuAlaLysLeuGlu 301
Db 913 AAGAGAAGAAAGAGCCGCAATATCTGACAGCGGAAAAAGCTTTTAGAACTCGCAAAATTGAG 972
QY 302 PheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLys 321
Db 973 TTCAACATCTTTCACCTCCCTTCAACAAGAGATTACAGTATCTCTCCAGATGTGATA 1032
QY 322 AspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeu 341
Db 1033 CATTCGGGTTTGCCCTGAACCTGACCTTTGGTCCGATCGTCACGTGAATACTACACCTTG 1092
QY 342 AlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMet 361
Db 1093 AGCTCTTGCACTTGCGACTGAGCCCAAACTTCTGCATTCAATTTGGGCTTGCCAAAACG 1152
QY 362 SerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeu 381
Db 1153 TGTCATCTTATCAGCGTTCTGAGCATATCTACGACACTTTCGGAACGATGATGAATC 1212
QY 382 GluLeuPheThrAlaThrIleLysArgTyrPaspProSerAlaMetGluCysLeuProGlu 401
Db 1213 GACTCTTCAACGAGGAGCAGTTAGAGATGGAATCCGTCGAGAAAGAACGCCCTCCAGAA 1272
QY 402 TyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAla 421
Db 1273 TATATGAAAGAAATCTCATGTGGCACTCTACGAAGCCTTACTGACATGGCGGAGAGGCA 1332
QY 422 GluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPhe 441
Db 1333 GAGAGACACAAAGCCGAGACACGCTCAATTAATGCTAGAAAGCCTTGGGAAGTTATCTT 1392
QY 442 AspSerTyrMetGlnGluAlaLysTyrIleAlaThrGlyTyrLeuProThrPheGluGlu 461
Db 1393 GATTCGTATACACAAGAACAAAGTGAATGCCAGCGGTTATCTGCCAACTTCGAGAG 1452
QY 462 TyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu 481
Db 1453 TACTTAGAAGAACGGAAGTTAGCTGTGTCATCGTGACGCGCATTTGACACCCCTCTGTG 1512
QY 482 ThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeu 501
Db 1513 ACATTGACGTACCGCTTCTCTGATGACGCTTGAAGGAATAGATTTTCCATCGAGATTT 1572
QY 502 AsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAsp 521
Db 1573 AATGATTTGGCATCTTCTCTTCTAGACTAAGAGGTGACACACGATGCTACAAAGGAGAC 1632
QY 522 ArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeu 541
Db 1633 AGGAGCCGAGAGAGAAAGCGTCAAGCATATCGTGTACATGAAGAACAATCCCGGATTA 1692
QY 542 ThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeu 561
Db 1693 ACAGAGGAAGATGCTCTCAATCATATCAATGCCATGATCAACGACATTAACAAGAAATTA 1752
QY 562 AsnTyrGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPhe 581
Db 1753 AATTGGAACTTCTCAAAACCCGATAGCAATATTCGAATGACTGCACGGAAACATGCTTAT 1812
QY 582 AspIleSerArgValTrpHisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsn 601
Db 1813 GAGATAACCAAGCTTTCACCACTTACAAATAATAGAGATGGCTTCAGCGTTGCCACT 1872



QY 602 ValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618  
Db 1873 CAAGAAACGAAAGTTTGTCAGAGAACGCTCCTTGAACCAAGTCCTCTT 1923

RESULT 9

US-09-887-586A-29  
; Sequence 29, Application US/09887586A  
; Patent No. US20020094556A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20020094556A1, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/887,586A  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/398,395  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Abies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)...(1949)  
; OTHER INFORMATION: myrcene synthase  
US-09-887-586A-29

Alignment Scores:  
Pred. No.: 6.3e-249 Length: 2196  
Score: 2200.50 Matches: 427  
Percent Similarity: 80.38% Conservative: 77  
Best Local Similarity: 68.10% Mismatches: 106  
Query Match: 67.69% Indels: 17  
DB: 9 Gaps: 7

US-10-025-145A-65 (1-618) x US-09-887-586A-29 (1-2196)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15  
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QY 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35  
Db 129 AGTTCAATTCATGAACATAAGCCCTCCCTATAGAACAATCCCAATCTTGGAATGCGTAGG 188  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
Db 189 CGAGGGAATCTGTCAACGCCCTTCATGAGCATCAGTTGGCCACCGCTGCACCTGATGAT 248  
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrPaspaspPheIleGln 75  
Db 249 GGTTGACAAAGACGATAGGTAAGTCAATTCATCAATATCTGGAGACGATGATTTCATACAG 308  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 309 TCTCTA--TCAACGCCCTTATGGGGAACCCCTTACCGAGAACGTGCTGAGAGATTAAATT 365  
QY 96 GlyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112  
Db 366 GTGAGGTAAAGAGATA--TTCAATTCAATGTACCTGATGATGAGAGATTAAATGACT 422  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuLeuValAspValGluArgLeuGlyIle 130  
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QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
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QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 543 GAAACGCGCATTTGATGTGGAGAGACAGATTTGTACTGATCTCACTCACTGCGTTG 602  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 603 GGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 662  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210  
Db 663 CAAGATCAAAATGGACAGTTGTATGCTCCCGCGT--CAGACAGAGGTCAGATCAGA 719  
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
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QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
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Db 1437 GCAAAATGATCTCTAATGTATTATCTGCCAATGTTGAAGAAGTACCATGAGAAATGGAAA 1496  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487  
Db 1497 GTAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCCTCACTTGAATGATGAGCTT 1556







QY 251 SerIleuSerIleuGluIleArgaspValIleuGluTyrGlyTyrPHisThrAsnIleuPro 270  
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QY 271 ArgIleuGluAlaArgasnTyrMetaspValPheGlyGlnHisThrIys-----Asn 287  
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QY 308 IeuGlnGluArgGluIleuIysHisValSerArgTTrpIlyaspSergIysSergIu 327  
Db 1017 TTACAACAAAAGGAATTACATATCTTTTGAGATGTTGGAAGAAGCTCGGATTGGCTTAA 1076  
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaIleuAlaSerCysIleAlaPhe 347  
Db 1077 TTGACATTGCTCGGCATGCTCATGTGGAATTCTACACTTTGGCCTCTGTATGGCATT 1136  
QY 348 GluProGlnHisSergIyPheArgIleuGlyPheThrIysMetSerHisIleuIleThrVal 367  
Db 1137 GACCCAAAACATTCTGCATTCAGACTAGAGCTTCGCCAAAATGTGTCACTCTGTACAGTT 1196  
QY 368 IeuaspSpmetTyraspValPheGlyThrValaspGluIleuGluPheThrAlaThr 387  
Db 1197 TTGACGATATTTCAGACACTTTTGAAACGATTGACGAGCTTGAACCTTCACATCTGCA 1256  
QY 388 IleIysArgTTrpaspProSeralMetGluCysIeuProGluTyrMetIysGlyValTyr 407  
Db 1257 ATTAAGAGATGGAATTTCATCAGAGATAAGAACCTTCAGAAATATATGAATGTGTAC 1316  
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluIysAlaGlnGlyArg 427  
Db 1317 ATGCTGCTGTTGAAACTGTAAATGAACGTGACACGAGAGCGGAGAGAAGACTCAAGGAGA 1376  
QY 428 AspThrIleuAsnTyrAlaArgGlnAlaTTrpGluAlaCysPheaspSergTyrMetGlnIu 447  
Db 1377 AACACTCTCAACTATGTTCGAAGCGCTTGGAGGCTTATTTGATTCATATATGGAAGAA 1436  
QY 448 AlaIysTrpIleAlaThrGlyTyrIleuProThrPheGluGluTyrIleuGluAsnGlyIys 467  
Db 1437 GCAAAATGATCTCTAATGGTTATCTGCCAATGTTTGAAGAGTACCATGAGAATGGGAAA 1496  
QY 468 ValSerseralHisArgProCysAlaIleuGlnProIleIleuThrIleuAspIleProPhe 487  
Db 1497 GTGAGCTGTCATATCGCGTAGCAACATTCGAACCCCATCTTCACTTTGAATGCATGGCTT 1556  
QY 488 ProAspHisIleuIysGluValaspPheProSergIysIleuAsnaspIleuIleCysIle 507  
Db 1557 CCTGATACATCTTGAAGGAATTGATTTCCATCCAGGTTCAATGATTTGGCATCTGCTCC 1616  
QY 508 IleIeuArgIleuArgGlyaspThrArgCysTyrIysAlaaspArgAlaargGlyGluGlu 527  
Db 1617 TTCCTTCGGCTACGAGGTGACACACGCTGCTACAAGCGCATAGGGGATCGGTGAAGAA 1676  
QY 528 AlaSergSerIleSergCysTyrMetIysaspasnProGlyIleuThrGluIuaspAlaIleu 547  
Db 1677 GCTTCGTGTAATCATGTTATATGAAGACAATCCTGGATCAACCGAAGAAGATGCCCTC 1736  
QY 548 AsnHisIleasnPheMetIleArgaspAlaIleArgGluIleuAsnTrpGluIleuIys 567  
Db 1737 AATCATATCAATGCCATGTGTCATGACATAATCAAGAATTAAATTGGGAATTCTTAAGA 1796  
QY 568 ProaspasnServalProIleThrSerIysIysHisAlaPheaspIleServalTTrp 587  
Db 1797 TCCAACGACAAATATTCGAATGCTGGCCAAGAAACATGCTTTTGACATTAACAAGAGCTCTC 1856  
QY 588 HisHisGlyTyrArgTyrArgaspGlyTyrSerPheAlaasnValGluThrIysSerIeu 607  
Db 1857 CACCATCTCTACATATATCGAGATGGCTTTAGTGTTCGCCAACCAAGGAACAAAAAATTG 1916  
QY 608 ValMetArgThrValIleGlu 614

Db 1917 GTTATGGAACACTCTTGAA 1937  
RESULT 12  
US-09-893-820-29  
; Sequence 29, Application US/09893820  
; Publication No. US20040053386A1  
; GENERAL INFORMATION:  
; APPLICANT: Chappell, Joseph  
; APPLICANT: No. US20040053386A11, Joseph P.  
; APPLICANT: Starks, Courtney M.  
; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SYNTHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/893,820  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US/09/398,395A  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,993  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/130,628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150,262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Adies grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)...(1949)  
; OTHER INFORMATION: myrcene synthase  
US-09-893-820-29  
Alignment Scores:  
Pred. No.: 6.3e-249 Length: 2196  
Score: 2200.50 Matches: 427  
Percent Similarity: 80.38% Conservative: 77  
Best Local Similarity: 68.10% Mismatches: 106  
Query Match: 67.69% Indels: 17  
DB: 13 Gaps: 7  
US-10-025-145A-65 (1-618) x US-09-893-820-29 (1-2196)  
QY 1 MetAlaIleuIeuSerIleThrProIleuValSerArgSergCysIeu----- 15  
Db 69 ATGGCTCTGCTTCTATCTCACCCTTGCTTGCAAAATCTTGCTCGCAAGTCGTGATC 128  
QY 16 SerSergSerHisGluIleIysAlaIleuArgArgThrIleProThrIleuGlyIleCysArg 35  
Db 129 AGTTCAATTCATGAACATAAGCCCTCCCTATAGAACAAATCTTGAATGCGTAGG 188  
QY 36 ProGlyIysServalAlaHisSerIleAsnMetCysIeuThrSerValAlaSerThrAsp 55  
Db 189 CGAGGAAATCTGTACGCTTCCATGAGCATCAGTTTGGCCACCGCTGCACCTGATGAT 248  
QY 56 ServalGlnArgArgValGlyAsnTyrHisSerAsnIleuTTrpaspaspPheIleGln 75  
Db 249 GGTGTACAAAGACGATAGGTGACTTCCATTCATTAATCTGGACGATGATTTCATACAG 308  
QY 76 SerIleIleSergThrProTyrGlyAlaProaspTyrArgGluArgAlaaspArgIleIle 95  
Db 309 TCTCTA--TCAACGCTTATGGGAACCTCTTACCAGGAACGTGCTGAGAGATTAAAT 365  
QY 96 GlyIuValIysaspIleMetPheAsnPhelysSerIeuGluaspGlyGly----- 112  
Db 366 GTGAGGTAAGAAGATA--TTCAATTCAATGTACCTGGATGATGAGAATTATGAGT 422  
QY 113 -----AsnaspIleuIeuGlnArgIleuIeuValaspValGluArgIleuGlyIle 130  
Db 423 TCCTTAATGATCTCATGCAACGCTTTGGATAGTCGATAGCGTTGAACGTTTGGGGATA 482



QY

131

AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn

150

Db

483

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542

QY

151

GIuLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu

170

Db

543

GAAACCGGCATTTGGATGTGGAGAGACAGATATTGTTACTGATCTCAACTCAACTGCCGTG

602

QY

171

GlyLeuArgThrLeuAlaGluLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe

190

Db

603

GGGTTTCAACTCTTGCAATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT

662

QY

191

LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIleArg

210

Db

663

CAAGATCAAAATGACAGTTTGATGCTCCCCCGGT---CAGACAGAGGCTGAGATCAGA

719

QY

211

GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp

230

Db

720

AGCGTTCTTACTATATCGGGCTTCCCTCATGGCTTCCCTGGTGAGAAAGTTATGGAA

779

QY

231

GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer

250

Db

780

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839

QY

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270

Db

840

GCT---CTTTCACAGAGATTAAGTTGTTATGGAATATGCTGGCACAAATTTGCCCA

896

QY

271

ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn

287

Db

897

AGATTGGAAGCAGAAATTTACATAGACACACTTGAAAGACACACAGTCGATGGCTCAAT

956

QY

288

LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer

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957

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308

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327

Db

1017

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1076

QY

328

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347

Db

1077

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1136

QY

348

GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal

367

Db

1137

GACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGCATCTTGTTCACAGTT

1196

QY

368

LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr

387

Db

1197

TTGGACGATATTTCAGACACTTTTGAACGATTGACGAGCTTGAACCTTTCACATCTGCA

1256

QY

388

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407

Db

1257

ATTAAAGATGGAATTTCATCAGAGATAGAACACCTTCCAGATATATGAATGTGTGTAC

1316

QY

408

MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg

427

Db

1317

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1376

QY

428

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447

Db

1377

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1436

QY

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1496

QY

468

ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe

487

Db

1497

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1556

QY

488

ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle

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1616

QY

508

IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu

527

Db

1617

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1676

QY

528

AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu

547

Db

1677

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1736

QY

548

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1796

QY

568

ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp

587

Db

1797

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1856

QY

588

HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu

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1857

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614

Db

1917

GTTATGGAACACTCCTTGAA 1937

1937

RESULT 13

US-10-041-007-25

Sequence 25, Application US/10041007

Publication No. US20020164736A1

GENERAL INFORMATION:

APPLICANT: Matsuda, Seichi P.T.

APPLICANT: Schepman, Hala G

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

FILE REFERENCE: P02081US1

CURRENT APPLICATION NUMBER: US/10/041, 007

CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: US 60/259, 881

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

LENGTH: 2196

TYPE: DNA

ORGANISM: Abies grandis

US-10-041-007-25

Alignment Scores:

Pred. No.: 6.3e-249

Score: 2200.50

Percent Similarity: 80.38%

Best Local Similarity: 68.10%

Query Match: 67.69%

DB: 14

Length: 2196

Matches: 427

Conservative: 77

Mismatches: 106

Indels: 17

Gaps: 7

US-10-025-145A-65 (1-618) x US-10-041-007-25 (1-2196)

QY

1

MetaLeuLeuSerIleThrProLeuValSerArgSerCysLeu-----

15

Db

69

ATGGCTGTGTTTCTATCTACCGTTGGCTTCGAAATCTTGCGTGCAGCAAGTCGTGATC

128

QY

16

SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg

35

Db

129

AGTTCAATTCAAGACATAAGCCTCCCTATAGAACAAATCCCAATCTTGAATGCGTAGG

188

QY

36

ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp

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Db

189

CGAGGGAATCTGTACGCCCTTCATGACATCAGTTTGGCCACCGCTGCACCTGATGAT

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75

Db 249 GGTGTACAAGACGCATAGCTGACTACCATTCCAATATCTGGGACGATGATTTTCATACAG 308  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
Db 309 TCTCTA--TCAACGCCTTAAGGGAAACCTCTTACCAGGAACGTGCTGAGAGATTAAATT 365  
QY 96 GlyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112  
Db 366 GTGAGAGTAAAGAAGATA--TTCAATTCAATGATACCTGGATGATGGAAGATTATGAGT 422  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130  
Db 423 TCCTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGGAATA 482  
QY 131 AspArgHisPhelysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
Db 483 GCATAGACATTTCAAGACGAGATAACATCAGCTCTGATTAATGTTTCCGTTACTGGGAG 542  
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
Db 543 GAAACGCGCATTTGGATGTGGAGAGACAGTATGTACTGATCTCAACTCAACTCGCGTTG 602  
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
Db 603 GGGTTTCGAACCTCTTCGATTACCGGTAACACTGTATCTCCAGAGGTTTAAAGCCTTTT 662  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210  
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QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230  
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QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
Db 780 GAAGCTGAATCTTCTCCACAAGATATTGAAGAAGCTCTACAAAGAATTCCAGTCTCC 839  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270  
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QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287  
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QY 288 LysAsnAlaAlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307  
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QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327  
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QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367  
Db 1137 GACCCAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCACTTGTCAAGATT 1196  
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387  
Db 1197 TTGACGATATTACGACACTTTTGGAAACGATTGACGAGCTTGAACCTTTCACATCTGCA 1256  
QY 388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
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QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427  
Db 1317 ATGTCGTGTTGAAAAGCTGTAATGAAGTACAGAGAGCGGAGAGAACTCAAGGGAGA 1376

QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnGlu 447  
Db 1377 AACACTCTCAACTATGTTGAAAAGCCTTGGAGGCGTTATTTTCATTATATATGGAAGA 1436  
QY 448 AlAlaSTripIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
Db 1437 GCAAAATGATCTCTAATGTTATCTGCCAATGTTTGAAGATAACCATGAGAATGGGAAA 1496  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487  
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCTCACTTGAATGCATGGCTT 1556  
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
Db 1557 CCTGATTACATCTTGAAGGAATGATTTTCCATCCAGGTTCAATGATTGGCATCGTCC 1616  
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527  
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QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547  
Db 1677 GCTTCGTATATCATGATGTATATGAAGAACAATCCTGATCAACCGAAGAAGATGCCCTC 1736  
QY 548 AsnHisIleAsnPhemetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567  
Db 1737 AATCATATCAATGCCATGTCATGACATATATCAAGAATTAATTGGGAACCTTCAAGA 1796  
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587  
Db 1797 TCCAACGACAATATTCCAAATGCTGGCCCAAGAAACATGCTTTTGACATACAAAGACTCTC 1856  
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607  
Db 1857 CACCATCTCATATATATGAGATGGCTTTAGTGTGCCAAACAAGAAAACAAAAAATTG 1916  
QY 608 ValMetArgThrValIleGlu 614  
Db 1917 GTTATGGAACACTCCTTGAA 1937

RESULT 14

US-10-025-145A-1  
; Sequence 1, Application US/10025145A  
; Publication No. US20030175861A1  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney B.  
; APPLICANT: Bohlmann, Joerg  
; APPLICANT: Steele, Christopher L.  
; APPLICANT: Phillips, Michael A.  
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
; FILE REFERENCE: WSUR118414  
; CURRENT APPLICATION NUMBER: US/10/025,145A  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/360,545  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: PCT/US98/14528  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: US 60/052,249  
; PRIOR FILING DATE: 1997-07-11  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Abies Grandis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)..(1952)  
; OTHER INFORMATION:  
; US-10-025-145A-1

Alignment Scores:

Pred. No.: 6.3e-249  
Score: 2200.50  
Percent Similarity: 80.38%  
Best Local Similarity: 68.10%  
Query Match: 67.69%  
DB: 15  
Length: 2196  
Matches: 427  
Conservative: 77  
Mismatches: 106  
Indels: 17  
Gaps: 7

US-10-025-145a-65 (1-618) x US-10-025-145a-1 (1-2196)

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Db      69 ATGGCTCTGTTCTATCTACCGCTTGCTTGAATCTTGCTGCGCAAGTCGTTGATC 128

QY      16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db      129 AGTTCAATTCATGAACATAAGCCTCCCTATAGAACATCCCAATCTTGGAATGCGTAGG 188

QY      36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db      189 CGAGGGAATCTGTCAAGCCTTCCATGAGCATCAGTTGGCCACCGCTGCACCTGATGAT 248

QY      56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db      249 GGTGTACAAGAAGCGCATAGTGACTACCATTCGAATATCTGGAGCGATGATTTCATACAG 308

QY      76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db      309 TCTCTA--TCAACGCCCTTATGGGGAACCTCTTACCAAGAACGTGTGAGAGATTAAAT 365

QY      96 GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly----- 112
Db      366 GTGAGGTAAAGAGATA--TTCAATTCATGTACCTGATGATGAGAATTAATGAGT 422

QY      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db      423 TCCTTTAATGATCTCATGCAACGCCCTTGAGTATGATAGCGTTGACGTTGGGGATA 482

QY      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db      483 GCTAGACATTTCAAGAACGAGATACATCAGCTCTGATTAATGTTTCCGTTACTGGGAG 542

QY      151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db      543 GAAACCGGCATTTGATGTGGGAGAGACAGATATTTACTGATCTCACTCAACTGCGTTG 602

QY      171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db      603 GGGTTTCGAATCTCTCGATTACACGGGTACTGTATCTCCAGAGGTTTAAAAAGCTTTT 662

QY      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210
Db      663 CAAGATCAAAATGGAACAGTTGTATGCTCCCGCGT--CAGACAGAGCGTGAATCAGA 719

QY      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db      720 AGCGTTCTTAATCTATATCGGCTTCCCTCATTTGCCCTTGCGTGAAGTATGGA 779

QY      231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db      780 GAAGCTGAATCTTCTCCACAGATATTTGAAAGAGCTCTACAAAAAGATTCCAGTCTCC 839

QY      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheHisThrAsnLeuPro 270
Db      840 GCT--CTTTCAACAAGATAAAGTTTGTATGGAATATGGCTGGCACACAAATTGGCA 896

QY      271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
Db      897 AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACAGTCATGGCTCAAT 956

QY      288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db      957 AAAAATGCTGGGAAGAGCTTTTAGAATTTGCAAAATTGAGATTCAATATATTTAACTCC 1016
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QY      308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db      1017 TTACAACAAGAAAGATTACATATCTTTGAGATGCTGGAAGAGTCGGATTTCCTAAA 1076

QY      328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db      1077 TTGACATTTGCTCGGCATCGTCATGTGAATTCTACACTTTGGCCTCTTGTAATGCCATT 1136

QY      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db      1137 GACCCAAAACATTCATTCAGACTAGGCTTGCCCAAAATGTGTCACTCTGTGCACAGTT 1196

QY      368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db      1197 TTGACGATATTTACGACACTTTTGGAACGATTGACGAGCTTGAACTCTTCACATCTGCA 1256

QY      388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db      1257 ATTAAGAGATGGAATTTCATCAGAGATAGAACACCTTCCAGATATATGAATGTGTAC 1316

QY      408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db      1317 ATGTCGTGTTTGAACCTGTAATGAACACTGACGAGAGCGGAGAAAGACTCAAGGAGA 1376

QY      428 AspThrLeuAsnTyrAlaArgGluAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db      1377 AACACTCTCACTATGTTTGGAAAGCGTTGGAGGCTTATTTGATTCAATATATGCAAGAA 1436

QY      448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db      1437 GCAAAATGATCTCTAATGTTATCTGCCAATGTTTGAAGAGTACCATGAGATGGGAAA 1496

QY      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db      1497 GTGAGCTCGCATATCGCGTAGCAACATTCGAACCCATCCTCACTTTGAATGATGGCTT 1556

QY      488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db      1557 CCTGATTACATCTTGAAGGAATTGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616

QY      508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db      1617 TTCCTTCGGCTACGAGGTGACACACGCTGCTACAAAGGCCGATAGGATCGTGTGAAGAA 1676

QY      528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db      1677 GCTTCGTATATCATGTTATATGAAGACAATCCTGATCAACCGAAGAAAGATGCCCTC 1736

QY      548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db      1737 AATCATATCAATGCCATGTCAATGACATAATCAAAAGATTAAATTGGGAACCTTCTAAGA 1796

QY      568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
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QY      588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
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QY      608 ValMetArgThrValIleGlu 614
Db      1917 GTTATGGAACACTCCTTGAA 1937

RESULT 15
US-10-025-145A-31
; Sequence 31, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
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TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)  
FILE REFERENCE: WSUR118414  
CURRENT APPLICATION NUMBER: US/10/025,145A  
CURRENT FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: US 09/360,545  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: PCT/US98/14528  
PRIOR FILING DATE: 1998-07-10  
PRIOR APPLICATION NUMBER: US 60/052,249  
PRIOR FILING DATE: 1997-07-11  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31  
LENGTH: 2205  
TYPE: DNA  
ORGANISM: Abies Grandis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (57)..(1943)  
OTHER INFORMATION:  
US-10-025-145A-31

Alignment Scores:  
Pred. No.: 1,44e-248 Length: 2205  
Score: 2197.50 Matches: 427  
Percent Similarity: 80.38% Conservative: 77  
Best Local Similarity: 68.10% Mismatches: 106  
Query Match: 67.59% Indels: 17  
DB: 15 Gaps: 7

US-10-025-145A-65 (1-618) x US-10-025-145A-31 (1-2205)

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QY 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35  
DB 117 AGTTCAATTCATGAACATAAGCCTCCCTATAGAACATCCCAATCTTGAATGCGTAGG 176  
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55  
DB 177 CGAGGGAATCTGTCAAGCCTTCCATGAGCATCAGTTGGCCACCGCTGCACCTGATGAT 236  
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrPaspAspPheIleGln 75  
DB 237 GGTGTACAAGACGCATAGGTGACTACCATTCATATCTGGGACGATGATTTCTATACAG 296  
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95  
DB 297 TCTCTA--TCAACGATTATGGGAAACCTCTTACCAGAAACGTCGAGAGATTAAATT 353  
QY 96 GLyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112  
DB 354 GTGAGGTAAGAGAGATA--TTCAATTCAATGTACCTGGATGATGAGATTAAAGAT 410  
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130  
DB 411 TCCTTTAATGATCTCATGCAACGCTTGGATAGTCGATAGCGTTGAACGTTGGGAGATA 470  
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150  
DB 471 GCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTCCGTTACTGGGAG 530  
QY 151 GLyLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170  
DB 531 GAAAAACGGCATTTGATGTGGGAGAGACAGATTTTACTGATCTCAACTCAACTGCCGTTG 590  
QY 171 GLyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190  
DB 591 GGGTTTCGAACCTTCGATTACACAGCGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 650  
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210

DB 651 CAAGATCAAAATGGACAGTTTGATGCTCCCGCGT---CAGACAGAGGGTGAGATCAGA 707  
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DB 708 AGCGTTCTTAATCTATATCGGGCTTCCCTCATTTGCCCTTCCTGGTGAAGAGTTATGGA 767  
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250  
DB 768 GAAGCTGAATCTTCTCCACAGATATTGAAAGAGGCTTACAAAAGATTCCAGCTCTCC 827  
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270  
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QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287  
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QY 288 LysAsnAlaAlaGlyLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307  
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DB 1125 GACCCAAACATCTTGCACTTACAGACTTACAGCTTCCGCAAAATGTGTCATCTGTACAGATT 1184  
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QY 388 IleLysArgTyrPaspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407  
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DB 1365 AACACTCTCACTATGTTGAAAGGCTTGGAGGCTTATTTGATTCATATATGGAAGAA 1424  
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467  
DB 1425 GCAAAATGGAATCTTAATGTTATCTGCAACGTTTGAAGAGATCAGATGAGAAATGGGAAA 1484  
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487  
DB 1485 GTGAGCTCTGCATATCGCGTAGCAACATGCAACCCATCCTCATTGATGCATGGCTT 1544  
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507  
DB 1545 CCTGATTACATCTTGAAGGGAATTGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1604  
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527  
DB 1605 TTCCTTGGCTACGAGGTGACACACGCTGCTACAAAGCCGATAGGGATCGTGTGAAGAA 1664  
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluAspAlaLeu 547  
DB 1665 GCTTGTGTAATCATGTTATATGAAGAGAAATCTGATCAACCGAAGAGATGCCCTTC 1724  
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTyrGluLeuLeuLys 567



Db	1725	AATCATATCAATGCCATGCTCAATGACATAATCAAGAATTAATTGGGA	CTTCTAAGA	1784
QY	568	ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgVal	Trp	587
Db	1785	TCCAACGACATATTCGATGCTGGCCAAGAAACATGCTTTTGACATAACAGAGCTCTC		1844
QY	588	HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSer	Leu	607
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QY	608	ValMetArgThrValIleGlu		614
Db	1905	GTTATGGAACACTCCTTGAA		1925

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Job time : 839 secs

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